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Mycobacterium tube
Mycobacterium tube
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Epstein Barr Virus
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Anti-sense strand
Vector pShuttle DN
Vector plasmid pCM
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Human brain expres
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Micromonospora DNA
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Human cDNA clone (
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                               AAQ14953
AAC15693
AAQ14952
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AAA10594
AAS81488
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AAS72787
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/*tag= a
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970S-0863079.
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23-MAY-1997;
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Granulin coding se
Human cancer assoc
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Mouse GP88 autocri
Mouse epithelin pr
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                                                                                                           Search time 457.59 Seconds (without alignments) 2352.554 Million cell updates/sec
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                                  Compugen Ltd.
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Copyright (c) 1993 - 2000
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                              This human cDNA sequence includes a coding region for GPBB (see AAMB5174), an 88 kDa glycoprotein autocrine growth factor and cepithilin/granulin precursor that is expressed in a tightly regulated manner in normal cells, is overexpressed and unregulated in highly tumorigenic cells derived from normal cells, and which acts as a stringently regulated growth stimulator for the tumorigenic cells. Inhibition of GPBB expression or action in the tumorigenic cells results in an inhibition of the tumorigenic cells results in an inhibition of the tumorigenic properties of the overproducing cells. Antagonists to GPBB are used to treat diseases associated with increased expression of GPBB, particularly cancer but all infections. Fragments of GPBB are used to raise specific antibodies (used as antagonists, as diagnostic reagents and for delivering toxins or other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ggaacgcggtgcccagatggtcagttctgccctgtggcctgctgcctggaccccggagga 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
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                                                                                                                                                                                                                                                                                                                           compounds to GP88-expressing cells) and to screen for antibodies. Antisense oligonucleotides can also be used as antagonists. Methods are provided for diagnosing disease, or determining susceptibility to disease, resulting from altered GP88 activity.
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                                                                                                       English.
                                                                                                       86pp;
                                                                                                       Disclosure; Fig 9A;
WPI; 1999-045276/04
                 P-PSDB; AAW85475
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misc_difference 1640..1642
/*tag = b
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11 Similarity 100.0%; Pred. No. 1.6e-154;
627; Conservative 0; Mismatches 0;
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                                     627
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BP.
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granulocytes; leucocytes;
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                                                                                                                                   DNA;
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            gtctcagggacttccagttgctgcccttcccagaggccgtggcatgcggggatggccat
                                                                                                                                                                                                                                                                                                                                                                                                                                                New cystine rich granulin peptide(s) from leucocyte(s) - are keratinocyte inhibitors useful topically for wound healing
                                                                                                                                                                                                                                                                  wound healing; inhibition; peptide;
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/transl_except= ATG encodes Valine.
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                                                                                                                                                                   Location/Qualifiers
1453..1455
/*tag= a
                                                                                                                                                                                                               DNA; 2198 BP
                                                                                                                                                                                                                                                                        granulocytes; leucocytes; ss
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                                                                                                                                                                                                                                                                                                                                                                                        92US-0829233
                                                                                                                                                                                                                                                     Granulin coding sequence.
                                                                                                                                                                                                                                                                  Granulin; keratinocytes;
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P-PSDB; AAR48673.
                                                                                                                                                                                                               AAQ49052 standard;
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misc_difference
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Human; cancer associated gene; cancer antigen; detection; cancer; diagnosis; cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral; antidiamatory; antityroid; antiallergic; antibacterial; cardiant; dermatological; neuroprotective; thrombolytic; coaquiant; nootropic; vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation; immune disorder; haematopoletic cell disorder; autoimmune disorder;
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     is useful in formulations
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                                                                   Length 2198
                                                                                      Indels
                                    BP; 398 A; 708 C; 646 G; 446 T; 0 other
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                                                                  ch 100.0%; Score 627; DB 14;
11 Similarity 100.0%; Pred. No. 1.6e-154;
627; Conservative 0; Mismatches 0;
      granulin inhibits keratinocytes and
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                  for promoting the healing of wounds
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                                      Sequence 2198
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                                                                   Query Match
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Matches 627
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAC77607 to AAC78448 encode the human cancer associated proteins given in AAB43388 to AAB44239. The proteins can have activities based on the tissues and cells the genes are expressed in. Example of activities antidabetic; antiasthmatic; unlearly; immunomodulator; antidabetic; antiasthmatic; antithround; antidabetic; antiasthmatic; antithround; antidabetic; antistratist, antidabetic; antipsoriatic and antidapetic; antiviral; dermatological; neuroprotective; cardiant; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic and antidapologenic. The present invention may be used for preventing, treating or ameliorating medical conditions and diagnosing pathological conditions. Colynucleotides, polypeptides, antibodies, agonists and antagonists from the present invention may be used to treat immune disorders by activating or inhibiting the proliferation, differentiation or mobilisation of disorders, allergic reactions, graft versus host disease and organ rejection, modulate haemostatic or thrombolytic activity, modulate inflammation, cancers, cardiovascular disorders, neurological disease and antagonists and antagonists may be also be used in the exemplification of the constitution of the case of 
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allergic reaction; graft versus host disease; organ rejection; haemostatic; thrombolytic; cardiovascular disorder; infection; neurological disease; drug screening; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 1097-1098; 2352pp; English
                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                          08-MAR-2000; 2000WO-US05882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the present invention.
                                                                                                                                                                                                                                                                                                                 WPI; 2000-587533/55.
P-PSDB; AAB43971.
                                                                                                                                                                                                                                                                                Rosen CA, Ruben SM;
                                                                                                      WO200055350-A1.
                                                                       Homo sapiens
                                                                                                                                                                                                            12-MAR-1999;
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416 gtctcagggacttccagttgctgcccttcccagaggccgtggcatgcggggatggccat 475
                                                                                                                                                              536 ggtaacaactccgtgggtgccatccagtgccctgatagtcagttcgaatgcccggacttc 595
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41..1819
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/note= "claim
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ET-1 and ET-2 were isolated from rat kidneys and their amino acid sequences determined. A full length rat ET cDNA was obtd. by screening a rat kidney cDNA library in lambda q110 with PCR generated ET probes.

These probes were also used to obtain the mouse ET gene (AAQ14340) from a mouse T-cell genomic library. ET DNA was also obtained from human sources (AAQ14330).

An anti-sense ribonucleic acid molecule complementary to the indicated fragment in the features is also claimed.

ET-1 is a bifunctional growth regulator, capable of stimulating the growth of some cell types while inhibiting the growth of others.

ET-2 is functionally similar to ET-1 w.r.t. growth inhibitory chicked acid the growth stimulatory activity characteristic of ET-1 and, in fact, antagonises this ET-1 activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13 atgtggaccctggtgagctgggtggccttaacagcagggctggtggtggaacgcggtgc 72
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 stimulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      See also AAQ14338-40, AAQ14952-53, AAR14328-9 and AAR15315-20
                                                                                                                                                                                                                                                                                                                                   New cysteine-rich growth modulating proteins, epithelins - us as inhibitors of neoplastic cell growth and to promote wound healing and treat psoriasis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1767 BP; 359 A; 499 C; 491 G; 418 T; 0 other;
growth regulation; inhibition;
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                                                                                           /note= "claim 19, page
                                                   Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 18; 97pp; English.
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Best Local Similarity 80.7
Matches 488; Conservative
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                                                                                                                                                                                                                                                                    Shoyab M, Plowman GD;
                                                                                                                                                                                                                                                                                                WPI; 1991-325168/44.
P-PSDB; AAR14325.
  RNA;
  ET; anti-sense
                                                                                                                                                                           03-APR-1991; "
                              Rattus rattus
                                                                                                                                                                                                     13-MAR-1991;
                                                                                                                                                                                                                 03-APR-1990;
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                                                                                  of
  ET DNA was also obtained from human sources (AAQ14339).
An anti-sense ribonucleic acid molecule complementary to the indicated fragment in the factures is also claimed.
ET-1 is a bifunctional growth regulator, capable of stimulating the growth of some cell types while inhibiting the growth of the property sills functionally similar to ET-1 is furct, in thibitiory bloactivity. In contrast, however, ET-2 is apparently not capable of eliciting the growth stimulatory activity characteristic of ET-1 and
                                                                                                                                                                                                                                            13 atgtggaccctggtgagctgggtggccttaacagcagggctggtggctggaacgcggtgc 72
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                                                                                                              in fact, antagonises this ET-1 activity.
See also AAQ14338-40, AAQ14952-53, AAR14328-9 and AAR15315-20
                                                                                                                                                                                          Length 1779;
                                                                                                                                                                                                                   Indels
                                                                                                                                                  Sequence 1779 BP; 304 A; 578 C; 547 G; 350 T; 0 other;
                                                                                                                                                                                       98.1%; Score 615; DB 12; L
100.0%; Pred. No. 2.1e-151;
ive 0; Mismatches 0;
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regulated manner in normal cells, is overexpressed and unregulated in highly tumorigenic cells derived from normal cells, and which acts as a stringently required growth stimulator for the tumorigenic cells. Inhibition of GPBB expression or action in the tumorigenic cells results in an inhibition of the tumorigenic cells results in an inhibition of the tumorigenic properties of the overproducing cells. Murine GPBB cDNA was isolated from the highly tumorigenic PC cell line CDNA library isolated from the highly tumorigenic PC cell line CDNA library peptides. Antagonists to GPBB are used to treat diseases associated with increased expression of GPBB, particularly cancer but also viral infections. Fragments of GPBB are used to raise specific antibodies (used as antagonists, as diagnostic reagents and for delivering toxins or other compounds to GPBB expressing cells) and to screen for antibodies. Antisense oligonucleotides cells and disease, antagonists. Methods are provided for diagnosing disease, or determining susceptibility to disease,
                                                                                                                                                                                                                                                                                                                                                                     gccagctacagctgctgccgtccccttctggacaaatggcccacaacactgagcaggcat 180
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epithilin/granulin precursor that is expressed in a tightly
                                                                                                                                                                                                                                                                                Pred. No. 2.7e-95;
0; Mismatches 127; Indels
                                                                                                                                                                                                                               Sequence 2137 BP; 443 A; 608 C; 583 G; 503 T; 0 other;
                                                                                                                                                                                                                                                                    DB 20;
                                                                                                                                                                                                                                                                    Score 400.8;
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Local Similarity 79.0%;
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                                                                                                                                                         552
                                                                                                                                                                               537
                                                                     factor GP88 - useful for
for diagnosing disease
                                                                                                                                                       373 gtgggtgccatccagtgccctgatagtcagttcgaatgcccggacttctccacgtgctgt
        cggggcttccactgcagtgcagacgggcgatcctgcttccaaagatcaggtaacaactcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This murine cDNA sequence includes a coding region for GP88 (a AAW85474), an 88 kDa glycoprotein autocrine growth factor and
                                                                                                                                                                                                                                                                                                                                                                                                                                        GP88; granulin; epithilin; mouse; growth factor; autocrine; cancer; viral infection; antagonist; therapy; diagnosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tagonist of growth diseases and also
                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse GP88 autocrine growth factor cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Composition containing antagonist of
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23-MAY-1997;
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Immunogenic portion of an ovarian carcinoma protein and the nucleic acid encoding it, useful for the diagnosis, prevention and treatment of
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                                                                                                                                                                                                                                                   The present invention describes an isolated polypeptide comprising an
                                                                  cggggcttccactgcagtgcagacgggcgatcctgcttccaaagatcaggtaacaactcc 372
                                                                                                                                                                                                                                                                                                                552
                                                                                                                                                                                        373 gtgggtgccatccagtgccctgatagtcagttcgaatgcccggacttctccacgtgctgt 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ovarian carcinoma; ovarian cancer; therapy; diagnosis; antigen; identification; cytostatic; gene therapy; vaccine;
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98US-0216003.
99US-0338933.
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23-JUN-1999;
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ET DNA was also obtained from human sources (AAQ14339).

ET 1 is a bifunctional growth regulator, capable of stimulating the growth of some cell types while inhibiting the growth of others. ET-2 is functionally similar to ET-1 w.r.t. growth inhibitory bloactivity. In contrast, however, ET-2 is apparently not capable of elliciting the growth stimulatory activity characteristic of ET-1 and, in fact, antagonises this ET-1 activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ccagatggtcagttctgccctgtggcctgctgcctggaccccggaggagccagctacagc 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ccagatgggcagttctgccctgttgcctgcttgaccagggaggaggagccaactacagc 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 atgigggtcctgatgagctggctggccttcgcgggcagggctggtagccggaacacagtgt 60
                                                                                                                    ET; anti-sense RNA; growth regulation; inhibition; stimulation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New cysteine-rich growth modulating proteins, epithelins - useful as inhibitors of neoplastic cell growth and to promote wound healing and treat psoriasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1767;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 390.4; DB 12; Length
Pred. No. 1.3e-92;
0; Mismatches 126; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1767 BP; 360 A; 503 C; 492 G; 412 T; 0 other;
                                                                                                                                                                                                                /*tag= a
/note= "claim 29, page 56"
                                                                                                                                                                               Location/Qualiflers
8..1774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 23; 97pp; English.
AAQ14340 standard; DNA; 1767 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62.3%;
78.8%;
                                                                                                                                                                                                                                                                                                                                                   910S-0083796.
                                                                                                                                                                                                                                                                                                                                                                                                 (BRIM ) BRISTOL-MYERS SQUIB
                                                                                                                                                                                                                                                                                                                      91WO-US02321
                                                            (first entry)
                                                                                         Mouse epithelin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 479; Conservative
                                                                                                                                                                                                           /*tag-
                                                                                                                                                                                                                                                                                                                                                                                                                              Shoyab M, Plowman GD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1991-325168/44.
P-PSDB; AAR14327.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                   13-MAR-1991;
03-APR-1990;
                                                                                                                                                     Mus musculus
                                                                                                                                                                                                                                                                                                                     03-APR-1991;
                                                                                                                                                                                                                                                           WO9115510-A
                                                          17-JAN-1992
                                                                                                                                                                                                                                                                                        17-0CT-1991
                                                                                                                                                                                Key
misc_RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local 3
                              AAQ14340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13
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            Ovarian carcinoma proteins, and polynuclectides encoding them, have cytostatic activity and can be used in gene therapy and vaccines. Ovarian carcinoma polypeptides, nucleic acids, antibodies and vaccines are useful for the prevention, diagnosis and treatment of cancer, preferably ovarian cancer. AAA69691 to AAA70077 and AAB12552 to AAB12557 represent human ovarian carcinoma polynucleotides and proteins used in
                                                                                                                                                                                                                                 cattgctgccacggggttccactgcaqtgcagacgggcgatcctgcttccaaagatca 360
                                                                                                                                                                                                                                                                                                                                                                         gtctcagggacttccagttgctgccccttcccagaggccgtggcatgcggggatggccat 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; primer; detection; diagnosis; antisense therapy; gene therapy;
  protein (or its variants)
                                                                                                                                                                                    91
                                                                                                                                                                                                                                                                                                                                                                                                                                          31
                                                                                                                                                                                                                                                                                                                           ctgggtggcccctgccaggttgatgcccactgctgccggccactcctgcatcttacc
                                                                                                                                                                                                                                                                                                                                                                                    GTCTCAGGGACTTCCAGTTGCTGCCCCTTCCCAGAGGCCGTGGCATGCGGGGATGCCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                        Length 561;
                                                                                                                                                               Indels
                                                                                                   Sequence 561 BP; 106 A; 178 C; 175 G; 102 T; 0 other;
                                                                                                                                       21;
                                                                                                                                     Score 381.2; DB 2
Pred. No. 2.5e-90;
                                                                                the exemplification of the present invention.
  Immunogenic portion of an ovarian carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (5'-primer) SEQ ID NO:3976.
                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ggtaacaactccgtgggtgccatcca 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGTAACAACTCCGTGGATGGCACCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
                                                                                                                                      60.8%;
99.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-JUL-2000; 2000EP-0116126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99JP-0248036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                     Ouery Match 60.8
Best Local Similarity 99.2
Matches 383; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RES INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAH07141 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HELI-) HELIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EP1074617-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lomo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAH07141;
                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                          181
                                                                                                                                                                                                                                                                                                                                                                      241
                                                                                                                                                                                                                                                                                                                                                                                            150
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The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an ioligonucleotide comprises a 3'-end sequence complementary to a polynucleotide which comprises a 3'-end sequence complementary to a polynucleotide which comprises a 3'-end sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                           the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13631 to AAH118742 represent human cDNA sequences; AAB92446 to AAH03639 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
                                                                                        Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       actgetetgeeggeeaeteetgeatetttaeegteteagggaetteeagttgetgeeeet 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 gocotgatagicagitogaatgocoggacticicoacgigotgigitaiggicgaigget 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yamamoto J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gccctgatagtcagttcgaatgcccggacttctccacgtgctgtgttatggtcgatggct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 757;
 Saito K, Ya
Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 757 BP; 139 A; 232 C; 217 G; 165 T; 4 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .4e-68;
                                                                                                                                                                                   Claim 1; SEQ ID 3976; 2537pp + CD ROM; English.
 Hayashi K, S
A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47.4%; Score 297.4;
99.7%; Pred. No. 2.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human cDNA sequence SEQ ID NO:15309
Nishikawa T,
T, Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 99.7
Matches 298; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the present invention
                                                     4PI; 2001-318749/34
                       Sugiyama
 Isoqai T,
                                                                                                                                                    Full-length CDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-JUN-2001
                     Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAH16370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 329
 a
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gecetgatagteagttegaatgeeeggaetteteeaegtgetgtgttatggtegatgget 240

181

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2 g

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therapy; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods, AMH0316 to AMH13628 and AMH13633 to AMH13642 represent human cDNA sequences; AAB92446 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence and an oligonuclectide comprising a sequence complementary to a polynuclectide which comprises a 3'-end sequence, where the oligonuclectide comprises at least 15 nuclectides and the combination of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes primer sets for synthesising 5602 full-length cDMAs defined in the specification. Where a primer set comprises: (a) an oligo-dr primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
                                                                                                                                                                                                                                                                                                                                                                  Yamamoto J;
                                                                                                                                                                                                                                                                                                                                                                  alto K, Ya
Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1630 BP; 285 A; 517 C; 489 G; 339 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                    Saito
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 8; SEQ ID 15309; 2537pp + CD ROM; English.
detection; diagnosis; antisense
                                                                                                                                                                                                                                                                                                                                                             oggal T, Nishikawa T, Hayashi K, S
Sugiyama T, Wakamatsu A, Nagai K,
                                                                                                                                                                                                 99JP-0248036.
99JP-0300253.
2000JP-0118776.
2000JP-0183767.
                                                                                                                                                                                                                                                                                    2000JP-0241899
                                                                                                                                                           28-JUL-2000; 2000EP-0116126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the present invention.
                                                                                                                                                                                                                                                                                                                          (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-318749/34.
                                                                                                                                                                                                                                                                                                                                                                Isogai T,
  primer;
                                          Homo sapiens
                                                                           EP1074617-A2
                                                                                                                                                                                                                                                                                  09-JUN-2000;
                                                                                                                                                                                                 29-JUL-1999;
27-AUG-1999;
                                                                                                                                                                                                                                         11-JAN-2000;
02-MAY-2000;
                                                                                                                   07-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                   Ishii S,
Human;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   significant structural homology. Two members of the epithelin family, EP-1 and EP-2, have been purified from natural sources, and cDNAs encoding these and several other members of the epithelin family have been isolated from rat (AAQ14338), human (AAQ1439), bovine (AAQ14952), murine (AAQ14340) and chicken (AAQ14953).

ET-1 is a bifunctional growth regulator, capable of stimulating ET-1 is a bifunctional growth regulator, appable of others.

ET-2 is functionally similar to ET-1 w.r.t. growth inhibitory bloactivity. In contrast, however, ET-2 is apparently not capable of eliciting the growth stimulatory activity characteristic of ET-1 and,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 cactccaccagctgtgatttggagcgcggggcgctgtgtgtcccctacgggggacgtcccc 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       epithelins appear to comprise several distinct members sharing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        451 tgggggtgctgccccatgccccaggcttcctgctgtgaagacagggtgcactgctgtccg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 tgggggttgttgccccatgccgngaggcgtgtgctgccggggatgaggagcactgctgtccc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          511 cacggigootteigogacetggiteacaceegeigeateacaceeacgggeaceeece
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New cysteine-rich growth modulating proteins, epithelins - useful as inhibitors of neoplastic cell growth and to promote wound healing and treat psoriasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                See also AAQ14338-40, AAQ14952-53, AAR14328-9 and AAR15315-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 341 BP; 53 A; 108 C; 120 G; 59 T; 1 other;
                                                                                                                                                                       88
                                                                                                                                                                    ET; growth regulation; inhibition; stimulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.4%; Score 59; DB 12;
52.2%; Pred. No. 4.9e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                     Chicken epithelin precursor (partial).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 25; 97pp; English.
                                 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antagonises this ET-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 62.2%;
nes 92; Conservative
                                                                                                                                                                                                                                                                                                                                             91US-0083796.
                                                                                                                                                                                                                                                                                                                                                                                                 (BRIM ) BRISTOL-MYERS SQUIB.
                                                                                                                                                                                                                                                                                                             91WO-US02321
                                 AAQ14953 standard; DNA; 341
                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                 Shoyab M, Plowman GD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1991-325168/44.
P-PSDB; AAR15427.
                                                                                                                                                                                                       Gallus domesticus.
                                                                                                                                                                                                                                                                                                             03-APR-1991;
                                                                                                   17-JAN-1992
                                                                                                                                                                                                                                                                                                                                               13-MAR-1991;
                                                                                                                                                                                                                                                                                                                                                               03-APR-1990;
                                                                                                                                                                                                                                         WO9115510-A.
                                                                                                                                                                                                                                                                           17-0CT-1991.
                                                                   AAQ14953;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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The epithelins appear to comprise several distinct members sharing significant structural homology. Two members of the epithelin family, EP-1 and EP-2, have been purified from natural sources, and CDNAs encoding these and several other members of the epithelin family have been isolated from rat (AAQ14338), human (AAQ14339), bovine, murine (AAQ14340) and chicken (AAQ14953).

ET-1 is a bifunctional growth regulator, capable of stimulating the growth of some cell types while inhibiting the growth of others.

ET-2 is functionally similar to ET-1 w.r.t. growth inhibitory bloactivity. In contrast, however, ET-2 is apparently not capable of eliciting the growth stimulatory activity characteristic of ET-1 and, in fact, antigonises this ET-1 activity.

See also AAQ14338-40, AAQ14952-53, AAR14328-9 and AAR15315-20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gatagtcagttcgaatgcccggacttctccacgtgctgtgttatggtcgatggctcctgg 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gggtgctgccccatgccccaggcttcctgctgtgaagacagggtgcactgctgtccgcac 513
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New cysteine-rich growth modulating proteins, epithelins - useful as inhibitors of neoplastic cell growth and to promote wound healing and treat psoriasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 48.6; DB 12; Length Pred. No. 0.003; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 539 BP; 99 A; 171 C; 163 G; 106 T; 0 other;
                                                                               ET; growth regulation; inhibition; stimulation; ss.
                                         Bovine epithelin precursor (partial)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 24; 97pp; English.
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Local Similarity 60.0%;
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                  Shoyab M, Plowman GD;
                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1991-325168/44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAR15426.
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17-JAN-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is one of a large number of 5' ESTS derived from mRNAS encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTS were prepared from total human RNAS or polyA+ RNAS derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAS and even in those cases where longer CDNA sequences have been obtained, the full 5' UTR is rarely included. S' ESTS are derived from mRNAS with intext 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTS are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures.
                                                                                                                                                                                                                                                                                                                 Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping; ss.
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Pred. No. 0.0006;
2; Mismatches 0;
                                                                                                                                                                                                                                                                       Human secreted protein 5' EST, SEQ ID NO: 19768.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 51 BP; 12 A; 25 C; 8 G; 4 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID 19768; 71pp + CD-ROM; English
                     Duclert A,
571 ctggcaaagaagctccctgcccagagga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          expression and secretion vectors.
                                                                                                                                            AAC15693 standard; cDNA; 51 BP
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Best Local Similarity 96.1%;
Matches 49; Conservative
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                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-500381/45.
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Homo sapiens

06-OCT-2000

AAC15693;

AAC15693

à g 26-FEB-1999;

NAME OF THE PROPERTY OF THE PR

06-SEP-2000,

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Gaps

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DNA encoding novel human diagnostic protein #30141.

(first entry)

13-FEB-2002

AAQ14952 standard; DNA; 539

14

RESULT

AAQ14952

537

ò a AAQ14952;

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Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
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Homo sapiens

WO200175067-A2

11-0CT-2001

30-MAR-2001; 2001WO-US08631.

31-MAR-2000; 2000US-0540217, 23-AUG-2000; 2000US-0649167.

(HYSE-) HYSEQ INC.

Tang YT; Drmanac RT, Liu C,

WPI; 2001-639362/73. P-PSDB; ABG30150 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity

Claim 1; SEQ ID No 30141; 103pp; English.

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical immaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polypucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 3729 BP; 691 A; 1150 C; 960 G; 928 T; 0 other;

ö Gaps ö Length 3729; 64; Indels Query Match 6.6%; Score 41.6; DB 23; Best Local Similarity 55.6%; Pred. No. 0.34; Matches 80; Conservative 0; Mismatches 64;

206 occactgotctgocggocactcctgoatcttacogtctdagggacttcdagttgotgcc 265 a à

3090 cetgecetggcagettetecetgtteacageageeteetetetgtteacgtageeteteet 3149 cetteccagaggecgtggeatgegggatggecateactgetgeecacggggettecact 325 셤 δ

266

326 gcagtgcagacgggcgatcctgct, 349 ŏ

cetgitcacacagectetectect 3173 3150

Job time: 10533 sec

Search completed: September 5, 2002, 18:30:01

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Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 2 Sequence 3 Sequence 3 Sequence 2 Sequence 2 Sequence 2

US-07-885-971-15 US-08-087-783A-15 US-08-194-08B-15 US-08-194-088-15 US-08-23-04648-15 US-08-23-463-14 US-08-522-269B-2 US-08-522-269B-2 US-09-294-923-2 US-08-522-269B-1 US-09-294-923-1 US-09-294-923-1 US-09-103-840A-2

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Sequence 2, A Sequence 1, A Sequence 34, A Sequence 1, Ap Sequence 1, Ap

US-09-103-840A-1 US-08-426-819A-34 US-08-776-271-1 US-09-215-035-1 US-09-135-994-1

ALIGNMENTS

Sequence Sequence

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Sequence 16, Application US/08991862

Sequence 16, Application US/08991862

GENERAL INFORMATION:

APPLICANT: Serrer of Ginette

TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS

TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS

CURRENT APPLICATION NUMBER: US/08/991,862

CURRENT FILING DATE: 1999-08-17

EARLIER FILING DATE: 1997-05-23

NUMBER OF SEQ ID NOS: 17

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 16

LENGTH: 2095
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LOCATION: (13)..(1791)
; OTHER INFORMATION: Nucleotide sequence of human granulin/epithelin; OTHER INFORMATION: precursor (human GP88). Human Granulin Genebank; OTHER INFORMATION: M75161.
US-08-991-862-16
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627; Conservative
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    NAME/KEY: CDS
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  Query Match
Best Local Si
Matches 627,
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US-07-668-648-3
US-08-429-998-3
US-08-431-333-3
PCT-US91-02321-3
US-08-668-648-1
US-08-431-333-1
US-08-431-333-1
US-08-991-862-1
US-08-991-862-1
US-08-68-648-5
US-08-68-648-5
US-08-431-333-5
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US - 08 - 431 - 333 - 9
US - 08 - 68 - 648 - 7
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Copyright (c) 1993 - 2000
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Maximum Match 100%
Listing first 45 summaries
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seq length: 2000000000
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DB 4; Length 2095; Indels

Score 627; DB 4; L Pred. No. 9.2e-157; Mismatches 0;

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                                                                                                                                                                                                                                                                    Sequence 3, Application US/07668648
Patent No. 5416192
GENERAL INFORMATION:
APPLICANT: Showman, Gregory D.
TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
TITLE OF INVENTION: BUDULATING PROTEINS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ANDRESECEPT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/668,648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5624-161-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                 601 aacagggcagtggccttgtccagctcg 627
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ATTORNEY/AGENT INFORMATION:
NAME: MISTOCK, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5524
TELEPHONE: (212)790-9090
TELEPHONE: (212)790-907
INFORMATION FOR SED ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1779 base pairs
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US-07-668-648-3
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US-07-668-648-3
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Patent No. 5885961
GENERAL INFORMATION:
APPLICANT: Showman, Gregory D.
TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
TITLE OF INVENTION: MODULATING PROTEINS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARRE: PATENTIA Release #1.0, Version #1.25
98.1%; Score 615; DB 1; L
100.0%; Pred. No. 1.3e-153;
ive 0; Mismatches 0;
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Query Match 98.1
Best Local Similarity 100.
Matches 615; Conservative
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STREET: 11
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US-08-429-998-3
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                                                                                                                                        Sequence 3, Application US/08431333
Patent No. 5565723
GENERAL INFORMATION:
APPLICANT: Showman, Gregory D.
TITLE OF INVENTION: RETHELINS: NOVEL CISTEINE-RICH GROWTH
TITLE OF INVENTION: MODULATING PROTEINS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
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CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/431,333

FILING DATE: J7-APR-1995

CLASSIFICATION NUMBER: US/08/48

PRICATION NUMBER: US/08/68,648

PRICATION NUMBER: US 07/668,648

PRILING DATE: J3-ARR-1991

ATONIEV AGENT INFORMATION:

NAME: MISTOCK, S. Leslie

REGISTRATION NUMBER: 5624-161-999

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION OF SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
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100.0%; Pred. No. 1.3e-153;
ilve 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                      ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Matches 615; Conservative
                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE TYPE: Kidney
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COUNTRY: USA
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; LOCATION:
US-08-431-333-3
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US-08-431-333-3
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                                                               PULGATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER; US 07/668,648
FILING DATE: 13-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624-161-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)790-9090
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/429,998
FILLIGATION DATE: 27-APR-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                               TELEFAX: (212) 869-9741
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 1779 base pairs
                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
TISSUE TYPE: Kidney
                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
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; LOCATION: 1..1779
US-08-429-998-3
                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: CDNA ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
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ORIGINAL SOURCE:
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GENERAL INFORMATION:
APPLICANT: Shoyab, Mohammed
APPLICANT: Plowman, Gregory D.
TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
TITLE OF INVENTION: MODULATING PROTEINS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC COMPATIBLE
COMPUTER: Elappy disk
COMPUTER: Elappy disk
COMPUTER: Elap PC-DOS/MS-DOS
SOTTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/02321
FILING DATE: 19910403
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: POOL, Brian W.
REGISTRATION NUMBER: 32,928
REFERENCE/DOCKET NUMBER: ON0071A-PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)728-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Bristol-Myers Squibb Company
STREET: 3005 First Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IELEFAX: (206)728-4800
IELEFAX: (206)448-4775
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1779 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: lines
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Patent No. 5416192
GENERAL INFORMATION:
APPLICANT: Shoyab, Mohammed
APPLICANT: Plowman, Gregory D.
TITLE OF INVENTION: MODULATING PROTEINS
TITLE OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                  Length 1779,
                                                                                                         Indels
                                                                                    98.1%; Score 615; DB 5; L4 100.0%; Pred. No. 1.3e-153; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Pennie & Edmonds
1155 Avenue of the Americas
   Homo sapiens
                                                                                    Query Match 98.1
Best Local Similarity 100.
Matches 615; Conservative
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TISSUE TYPE: Kidney
FEATURE:
                                          1..1779
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New York
                               ; NAME/KEY: CDS
; LOCATION: 1...1
PCT-US91-02321-3
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133 tgctgccgtccccttctggacaaatggcccacaacactgagcaggcatctgggtggcccc 192
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                                                                                                                                                                                                                                      Gregory D. EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 406.6; DB 2;
Pred. No. 1.4e-98;
0; Mismatches 114;
                                                                                                                                                                                                                                                                        MODULATING PROTEINS
                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155. Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/668,648
FILING DATE: 13-MAR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/429,998
FILING DATE: 27-APR-1995
CLASSIFICATION: 514
                                                                                                                                                                Sequence 1, Application US/08429998
Patent No. 5885961
GENERAL INFORMATION:
APPLICANT: Shoyab, Mohammed
APPLICANT: Plowman, Gregory D.
TITLE OF INVENTION: EPITHELINS: NC
TITLE OF INVENTION: MODULATING PRO
                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 56:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 64.8%;
Best Local Similarity 80.7%;
Matches 488; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (212) 869-9741
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: doub
                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
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US-08-429-998-1
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COUNTRY:
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                             COMPUTER READABLE FORM:
MEDIUM TYEE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/668,648
FILING DATE: 19910019
CLASSIFICATION: 514
ATTORNEY,AGENT INFORMATION:
NAME: MISTOCK, S. Leslie
REGISTRATION NUMBER: 5624-161-999
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 780-9090
TELEPHONE: (212) 869-9741
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
LENGTH. 1767 base pairs
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 406.6; DB 1;
Pred. No. 1.4e-98;
0; Mismatches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 64.8%;
Best Local Similarity 80.7%;
Matches 488; Conservative
               ZIP: 10036
COMPUTER READABLE FORM:
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TOPOLOGY: 11n
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LOCATION:
US-07-668-648-1
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312
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                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/08431333
Patent No. 5965723
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Sloyab, Mohammed
APPLICANT: Plowman, Gregory D.
TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
TITLE OF INVENTION: MODULATING PROTEINS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Misrock, S. Leslie
REGISTRATION UNBER: 18,872
REFERENCE, DOCKET UNDER: 5624-161-999
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/668,648
FILING DATE: 13-MAR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/431,333
FILING DATE: 27-ARR-1995
CLASSIFICATION: 536
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TELEPRAX: (212)869-9741
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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133 tgctgccgtcccttctggacaaatggcccacaacatgagcaggcatctgggtggccc 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1767;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 1.4e-98;
0; Mismatches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 406.6;
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ADDRESSEE: Bristol-Myers Squibb Company
STREET: 3005 First Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application PC/TUS9102321
GENERAL INFORMATION:
APPLICANT: Shoyab, Mohammed
APPLICANT: Plowman, Gregory D.
TITLE OF INVENTION: EPITHELINS: NOVEL CY
TITLE OF INVENTION: MODULATING PROTEINS
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64.8%;
80.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 80.7
Matches 488; Conservative
TYPE: nucleic acid
STRANDENNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                1..1767
                                                                                                                                                                                                                                                                 CDS
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                                                                                                                                                                                                                                                   NAME/KET:
LOCATION:
US-08-431-333-1
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191 ctagatggctcctgccagacccatggccactgtcctgctggctattcttgtcttctcact 250
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                                                     11 cgcagacagaccatgtgggtcctgatgagctggctggccttcgcggcagggctggtagcc 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (23)...(1789)
OTHER INFORMATION: The sequence is identical to that of the published OTHER INFORMATION: mouse granulin except for one nucleotide (T OTHER INFORMATION: instead of G) at position 1071 of GP88 cDNA OTHER INFORMATION: (position 1056 of mouse granulin).
                                                                                                                                                                                                                                                                                                     APPLICANT: Serrero, Ginette
TITLE OF INVENTION: 88 KDA TUONRIGENIC GROWTH FACTOR AND ANTAGONISTS
TITLE OF INVENTION: 88 KDA TUONRIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 29996-488/P001-A
CURRENT APPLICATION NUMBER: US/08/991,862
EARLIER APPLICATION NUMBER: 08/863,862
EARLIER APPLICATION NUMBER: 09/863,862
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PALENTIN OFF. 2.0
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Length 2137;
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Pred. No. 1.4e-96;
0; Mismatches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Mouse epithelin/granulin
                                                                                                                                                                                                                                                  ; Sequence 1, Application US/08991862
; Patent No. 6309826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 63.7%;
Best Local Similarity 78.9%;
Matches 489; Conservative
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                                                                                                                            617
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US-08-991-862-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 406.6; DB<sub>1</sub>5;
Pred. No. 1.4e-98;
0; Mismatches 114;
                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
GURRENT APPLICATION DATA:
FILING DATE: 19910403
                                                                                                                                                                                             CLASSIFICATION: 514
ATTORNET/AGENT INFORMATION:
NAME: POOT, Brian W.
REGISTRATION NUMBER: 32,928
REFERENCE/DOCKET NUMBER: 0N0071A-PC
TELECOMMUNICATION INFORMATION:
TELEFAX: (206)728-4800
TELEFAX: (206)744-4775
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHRACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 64.8%;
Best Local Similarity 80.7%;
Matches 488; Conservative
                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1767 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE TYPE: Kidney
                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ORIGINAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1..1767
         Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
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PCT-US91-02321-1
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553 cccacgggcacccacccctggcaaagaagctccctgcccagaggactaacagggcagtg 612
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                                                                                                                                                                                                                                                                                                                                                                     301 CAGGGCTTCCACTGTAGTGCAAATCCTGCTTCCAGATGTCAGATAACCCCT-- 358
                                                                                                                                                                                                                                                                                                                                                                                                             373 gigggigccaiccagigcccigatagicagitcgaaigcccggactictccacgigcigi 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  478 AGAGTGCATTGCTGTCCCCATGGGGCCTCCTGTGGCTTCACACGATGCGTTTCA 537
                                                                                                       493 agggtgcactgctgtcgcacggtgccttctgcgacctggttcacacccgctgcatcaca
                                                                                  tgctgccgtccccttctggacaaatggcccacaacactgagcaggcatctgggtggcccc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application US/08429998
Patent No. 5885961
GENERAL INFORMATION:
APPLICANT: Shoyab, Mohammed
APPLICANT: Showman, Gregory D.
TITLE OF INVENTION: BPITHELINS: NOVEL CYSTEINE-RICH GROWTH
TITLE OF INVENTION: MODULATING PROFIENS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/429,998
FILING DATE: 27-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 07/668,648 FILING DATE: 13-MAR-1991 ATTORNET/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: New York STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           613 gccttgtc 620
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ZIP: 10036
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                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Shoyab, Mohammed
APPLICANT: Plowman, Gregory D.
TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
TITLE OF INVENTION: MODULATING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/668,648

FILING DATE: 19910819

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: MASTOCK: S. Leslie

REGISTRATION NUMBER: 18,872

REGISTRATION NUMBER: 18,872

REGISTRATION NUMBER: 16,999

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)790-9990

TELEPHONE: (212)790-9090

TELEPHONE: (212)790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 390.4; DB 1;
Pred. No. 2.7e-94;
0; Mismatches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/07668648
Patent No. 5416192
                                                                                                                                                                                                                         601 aacagggcagtggccttgtc 620
                                                                                                                                                                                                                                                             608 aacagcgcagtgtctttgcc 627
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Best Local Similarity 78.8%;
Matches 479; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGINAL SOURCE:
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: NUCLEIC ACID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
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; LOCATION:
US-07-668-648-5
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US-07-668-648-5
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                                                                                  EPITHELINS: NOVEL CYSTEINE-RICH GROWTH MODULATING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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Pred. No. 2.7e-94;
0; Mismatches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: MISTOCK, S. LESIIG
REGISTRATION NUMBER: 18,872
REGISTRATION NUMBER: 5624-161-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)790-9090
TELEFAX: (212)7869-9741
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION $\times \text{WBRE} \text{WBRE} \text{VBV} \text{MBRE} \text{TLSNE} \text{CARE} \text{CA
                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                          Gregory D.
                                                                                                                                                                                               ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the ?
CITY: New York
STATE: New York
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TISSUE TYPE: Kidney
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Best Local Similarity 78.8
Matches 479; Conservative
  GENERAL INFORMATION:
APPLICANT: Shoyab, Mohan
APPLICANT: Plowman, Gree
TITLE OF INVENTION: EPIT
TITLE OF INVENTION: MODI
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
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EDNESS: single
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COMPUTER READABLE FORM:
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MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
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; LOCATION: 1..1
US-08-431-333-5
                                                                                                                                                                                                                                                                                                                  USA
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Best Local Similarity 78.8%; Pred. No. 2.7e-94;
Matches 479; Conservative 0; Mismatches 126;
     5624-161-999
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US-08-431-333-5
; Sequence 5, Application US/08431333
; Patent No. 5965723
REFERENCE/DOCKET NUMBER: 5624
TELECOMUNICATION INFORMATION:
TELEPHONE: (212)790-9090
TELEFAX: (212) 869-9741
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1767 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                            ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                           TISSUE TYPE: Kidney FEATURE:
                                                                                                                                                                                                                                                                                    MOLECULE TYPE: CDNA ORIGINAL SOURCE:
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; LOCATION:
US-08-429-998-5
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             301 CAGGGCTTCCACTGTAGTGCAGATGGGAAATCCTGCTTCCAGATGTCAGATAACCCCT-- 358
                                                           AGAGTGCATTGCTGTCCCCATGGGGCCTCCTGTGACCTGGTTCACACACGATGCGTTTCA
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                                             gtgggtgccatccagtgccctgatagtcagttcgaatgcccggacttctccacgtgctgt
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application PC/TUS9102321
GENERAL INFORMATION:
APPLICANT: Shoyab, Mohammed
APPLICANT: Plowan, Gregory D.
TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
TITLE OF INVENTION: ADDILATING PROTEINS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/02321
FILING DATE: 19910403
APPLICALLOS
PILLING DATE: 19910403
CLASSIPICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: POOR, Brian W.
REGISTRATION NUMBER: 32,928
REGISTRATION NUMBER: 0N0071A-PC
TELECOMMUNICATION INFORMATION:
"FT. REPHONE: (206)728-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3: Bristol-Myers Squibb Company 3005 First Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
 1767 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (205)448-4775
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE TYPE: Kidney
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Washington
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598 TCTTTGCC 605
                                                                                                                                                                                                                                                                                613 gccttgtc 620
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LOCATION:
PCT-US91-02321-5
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PCT-US91-02321-5
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Length 1767;

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62.3%; Score 390.4; DB

Query Match

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                                                                                                                                                                73 ccagatggtcagttctgccctgtggcctgctgcctggaccccggaggagccagct@cagc 132
                                                                      13 atgtggaccctggtgagctgggtggccttaacagcagggctggtggctggaacgcggtgc 72
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                                                                                                                 1 ATGTGGGTCCTGATGAGCTGGCTGGCTTCGCGGCTGGTGGTGGTGTGT
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GENERAL INFORMATION:
APPLICANT: Shoyab, Mohammed
APPLICANT: Plowman, Gregory D.
TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
TITLE OF INVENTION: MODULATING PROTEINS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE BLISTOL-MYPER SQUIBD COMPANY
                        Indels
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  Pred. No. 2.7e-94;
); Mismatches 126;
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3005 First Avenue
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MEDIUM TYPE: Floppy disk
CONPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
  ilarity 78.8%;
Conservative
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CITY: Seattle
STATE: Washington
COUNTRY: USA
Best Local Similarity
Matches 479; Conserv
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PCT-US91-02321-9
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ATTORNEY/AGENT INFORMATION:

NAME: POOT, Brian W.

REGISTRATION NUMBER: 32,928

REFERENCE/DOCKET NUMBER: 000071A-PC

TELECHONE (206)728-4800

TELEPHONE: (206)748-4775

INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHRACTERISTICS:
LENGTH: 341 base pairs
TYPE: NUCLEIC ACID
STRANDEDENESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
ORGANISM: Gallus domesticus
TISSUE TYPE: Kidney
FATURE:
NAME/KEY: CDS

LOCATION: 1.339

PCT-US91-02321-9
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0; Gaps Length 341; Score 59; DB 5; Length 341 Pred. No. 5.8e-07; 0; Mismatches 56; Indels Query Match 9.4%; Best Local Similarity 62.2%; Matches 92; Conservative

451 tgggggtgctgcccatgccccaggcttcctgctgtgaagacagggtgcactgctgtccg 510 õ

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64 CACTCCACCAGCTGTGATTTGGAGCGCGGCGCTGTGTGTCTCCCTACGGGGACGTCCCC 123

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Search completed: September 5, 2002, 18:22:11 Job time: 13334 sec

Title: Perfect score:

sequence:

OM nucleic

Run on:

Scoring table:

Searched:

Database :

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BG469904 602533366
BF312609 603183187
BRM45957 603183187
BM045957 603634988
AL525926 AL525926
AU137266 AU137266
AU1339905 AU12484
AU133995 AU124912
AU12545 AU124945
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BF725386
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tissue was pooled from 10 individuals ranging in age from
4-80 years and RNA was extracted. From this pooled sample
an aliquot of 60w fortal RNA yielded 2.17ug of mRNA. A
directionally cloned cDNA library in the pCMVSPORT6 vector
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AL551350 AL551350
BF312922 601896379
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           AU132413 AU132413
BI755355 603024959
BG831133 602766695
                                                                                  ALS57765 ALS57765
BM051032 603633916
BG823225 602726592
                                                           BM009189 603629579
BM007370 603616596
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BG830081 602764827
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1 (bases 1 to 653)
14 (bases 1, Mernstein, S., Behal, A. and Smith, D. Wilstow, G.J., Bernstein, S., Behal, A. and Smith, D. WILBANK: EST analysis and bioinformatics for ocular genomics Invest. Ophthalmol. Vis. Sci. 41 (2000) In press
                                                  AU125816 AU125816
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National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
TEL: 301 402 3452
Fax: 301 496 0078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: graeme@helix.nih.gov
Plate: 15 row: c column: 09
Seq primer: M13RP1 reverse primer (ABI).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
                      BI755355
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/dev_stage="Adult"
/lab_host="EMDH108"
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AUTHORS
TITLE
JOURNAL
COMMENT
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BF725386
LOCUS
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  BF725386 bx15c09.y
AU121637 AU121637
AU130279 AU130279
BI771292 G03054655
BG682231 G02629538
BM010556 G03631748
                                                                                    ; Search time 3259.55 Seconds (without alignments) 2596.245 Million cell updates/sec
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AL542702 AL542702
BM468512 AGENCOURT
BM478783 AGENCOURT
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             GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                              13736207 segs, 6748477542 residues
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                                                                                       September 5, 2002, 13:08:22
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Maximum Match 100%
Listing first 45 summaries
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Score

Result

627 627 627 627 627 627 627 627 627 627

Vertebrata; Euteleostomi;

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421
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                             AUTHORS
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was constructed at Life Technologies, essentially following the protocols of the SuperScript Plasmid System full details of which are contained in the manufacturer's Instruction manual (http://www.lifetech.com/). First strand synthesis was carried out using a Not I primer-adapter [5'-pocTradParcTradAprGGGGGGGGGCGCCC(T)15-3']. Not I/blunt end inserts, were cloned into the Not I/FcoR V sites in the vector. EST analysis was performed on the unamplified allbrary at the NIH Intramural Sequencing Center (NISC).
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                                                                                                                    Length 653;
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                                                                                                                  Score 627; DB 10;
Pred. No. 8.3e-135;
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Email: genomics@hri.co.jp

HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix

Research Institute; cDNA library construction: Department of

Virology, Institute of Medical Science, University of Tokyo, and

Helix Research Institute.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 730)
Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y.,
Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and
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1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
151-1 81-438-52-3951
Fax: 81-438-52-3952
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 627; DB 9; I
Pred. No. 8.6e-135;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                 gland"
                                                                                                                                                                                                                                                                                                                                 /clone="MakWal00655"
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/ 240 c 220 g 148 t
                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
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                                                                                    HRI human cDNA project
Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
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Matches 627; Conservative
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Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genomics Laboratory
Helix Research Institute
153-3 Yana, Kisarazu, Chiba 292-0812, Japan
153-3 Yana, Masarazu, M
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100.0%; Pred. No. 8.7e-135;
ive 0; Mismatches 0;
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HRI human cDNA project
Unpublished (2000)
Contact: Takao Isogai
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 782)

NIH-MGC http://mgc.noi.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Onpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://mage.llnl.gov

Plate: LLAM11511 row: n column: 13

High quality sequence stop: 775.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BI771292 782 bp mRNA linear EST 25-SEP-2001
603054655F1 NIH_MGC_122 Homo saplens cDNA clone IMAGE:5204172 5',
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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/clone_lib="NIH_MGC_122"
/lab_host="DH10B"
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Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 785)

S NIH-MGC http://mgc.nci.nih.gov/.

S NIH-MGC http://mgc.nci.nih.gov/.

L Onpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Tissue Procurement: James Cleaver; M.D.

CONA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics) Inc.

Clone distribution: MGC clone distribution information can be
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                     Gaps
                                     GTCTCAGGGACTTCCAGTTGCTGCCCCTTCCCAGAGGCCGTGGCATGCGGGGATGGCCAT
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                                                                              /organism="Homo sapiens"
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/nab_host="ball08 (Til phage) resistant)"
/note="organ: skin; Vector: pcWV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.5kb. Library constructed by Life Technologies. Note: this is a NCI_CGAP Library."

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found through the I.M.A.G.E. Consortium/LLML http://image.lnl.gov Plate: LLAMI0615 row: k column: 10 High quality sequence stop: 783. Location/Qualifiers
                                                                                                                                                                                                                                                                                  tch 100.0%; Score 627; DB 10; al Similarity 100.0%; Pred. No. 8.8e-135; 627; Conservative 0; Mismatches 0;
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Best Local S:
Matches 627
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551 9

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/cell_type="teratocarcinoma"
/cell_line="NT2"
/note="Vector: pME18SFL3; mRNA from NT2 neuronal precursor cells after 7.00 sets retinoic acid (RA) induction"
267 c 237 g 166 t 5 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 814)
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Tel: 81-438-52-3951
Fax: 81-438-52-3955
Email: genomics@firi.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ota'T., Nishikawa'T., Suzuki,Y., Ishli,S., Saito,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
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                                     541 cgctgcatcacacccacgggcacccacccctggcaaagaagctccctgcccagaggact
                                                                                                                                                                                                          Length 814;
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/clone="NT2RP3000775"
/clone_llb="NT2RP3"
                                                                                                                                                                                                                                                                                       612 AACAGGGCAGTGGCCTTGTCCAGCTCG 638
                                                                                                                                                                                                                                                                   601 aacagggcagtggccttgtccagctcg 627
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Contact: Takao Isogai
Genomics Laboratory
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1 (bases 1 to 805)

NIH-MGC http://mgc.ncl.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Onpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: DCTD/TPP

CDNA Library Preparation: Ling Hong/Rubin Laboratory

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Likr at:

Http://image.linl.gov

Plate: LLCM1933 row: o column: 11

High quality sequence stop: 761.

Kigh quality sequence stop: 761.

Kigh quality sequence stop: 761.

All 1. :805

//clone="IMAGE:5448418"

//clone="IMAGE:5448418"

//clone="IMAGE:5448418"
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/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: poTB7; Site_1: XhoI; Site_2:
ECORI: cDNA made by oligo-dT priming Directionally cloned
into ECORI/XhoI sites using the following 5' adaptor:
GGCACGAG(GG, Library constructed by Ling Bnog in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
NIMB_MGC Library.

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mRNA sequence.
BM010556
BM010556.1 GI:16524910
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603055352F1 NIH_MGC_122 Homo saplens cDNA clone IMAGE:5204797 5',
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Mammalia; Eutheria; Primates; Catarihini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Tissue Produrement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://mage.llnl.gov

Plate: LLAM11513 row: h column: 14

High quality sequence stop: 843.
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gtctcagggacttccagttgctgcccttcccagaggccgtggcatgcggggatggccat
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NIH.MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
Unpublished (1999)
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/clone="IMAGE:2204797"
/clone_lib="NIH_MGC_122"
/lab_host="DH108"
/note="Organ: pooled lung ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
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Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 24 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for [iii]-length clones and was constructed by C. Gruber (Iniltrogen). Research Genetics tracking cgde 026. Note this is a NIH_MGC Library."
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Homo sapiens cDNA clone NT2RP3002089 5', mRNA
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100.0%; Pred. No. 9e-135;
Wiematches 0;
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AU131158 NT2RP3
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KEYWORDS
SOURCE
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a 279 c 248 g 175 t 4 others
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                                                                                                                                                                                                                   Email: genomics@hri.co.jp

HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix

Research Institute; cDNA library construction: Department of

Virology, Institute of Medical Science, University of Tokyo, and

Helix Research Institute.
                                Ota'T., Nishikawa'T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Nakamura,Y.', Nagai,T., Sugano,S. and
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                                                                                                                                                                     Japan
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                                                                     Isogal, T.
HRI human cDNA project
URDpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
Hellx Research Institute
H532-3 Yana, Kisarazu, Chiba 292-0812, Jag
Tel: 81-438-52-3951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tch 100.0%; Score 627; DB 9; al Similarity 100.0%; Pred. No. 9e-135; 627; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                          1. .849
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                   (bases 1 to 849)
                                                                   Isogai, T.
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cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)*
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                                                                                                                                                                                                                      BG823258 880 bp mRNA 11near EST 22-MAY-2001
602726638F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4866201 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIH-MGC http://mgc.ncl.nih.gov/.

National institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC
CONA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: NIH Intramural Sequencing Center
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llni.gov
Plate: LLCM732 row: 1 column: 10
High quality sequence stop: 855.
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalid; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 880)
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                                                                  BG823258.1 GI:14170845
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AL561424 LTI_NFL010_BC2 Homo sapiens cDNA clone CSODL007YF12 5
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
                                                                                                                                                                                       240
                                                                                                                                                                                                                                      480
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             Gaps
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                                                                                                                                                                                       Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EWRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
                                    tgctgtgaagacagggtgcactgctgtccgcacggtgccttctgcgacctggttcacacc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    518 TGCTGTGABGACAGGGTGCACTGTCTCTCCGCACGGTGCCTTCTGCGACCTGGTTCACACC
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             Indels
 Pred. No. 9.3e-135;
Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prime, mRNA sequence.
AL561424
AL561424.1 GI:12908842
 100.08;
              Conservative
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 Similarity
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              627;
Best Local S
Matches 627
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was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco FV sites of the pCMV5PORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
Email: filang@lifetech.com URL:
http://dillengdh.invitrogen.com"
/ Athere
                                                                                                                                                                                                                                                                                                                                                                                           AL552664 LTL_NFL006_PL2 Homo saplens cDNA clone CS0DI067YM23 5 prime, mRNA sequence.
AL552664 LT GI:12891784
EST.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 920)
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                                                                           cactgctgcccacggggcttccactgcagtgcagacgggcgatcctgcttccaaagatca 360
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Email: seqrefégenoscope.cns.fr, Web : www.
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//issue_type="B cells from Burkitt lymphoma"
//issue_type="B cells from Burkitt lymphoma"
//issue_type="B cells from Burkit lymphoma lymphoma dispersed with Not I and cloned into the Not I and Eco RV sites of the pcWvSpORT 6
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Matches 627; Conservative 0; Mismatches 0;
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/db_xref="taxon:9606"
/clone="Colorary 12017"
/clone=lib="LTI_NELO6_PL2"
/tissue_type="Placenta"
/rissue_type="Placenta"
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Email: seqreféqenoscope.cns.fr, Web : www.genoscope.cns.fr.
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Lill-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
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AL542702 LIL_FL002_PL1 Homo sapiens CDNA clone CSOBE011XC02 5 prime
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville (Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliangelifetech.com URL:
                                                                                                                                                                                                  313 CACTGCTGCCCACGGGCTTCCACTGCAGACGGGCGATCCTGCTTCCAAAGATCA 372
                                                                                                                                 ggtaacaactccgtgggtgccatccagtgcctgatagtcagttcgaatgcccggacttc 420
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
                               253 GICTCAGGGACTICCAGTIGCTGCCCCTTCCCAGAGGCCGTGGCATGCGGGATGGCCAT
                                                                cactgetgeccacggggettecactgcagtgcagacgggcgatectgettecaaagatea
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Unpublished (2001)
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/organism="Homo sapiens"
/db_xref='taxon:9606"
/clone='InAGE:5578048"
/clone='InAGE:5578048"
/tissue_type='melanotic melanoma"
/tasue_type='melanotic melanoma"
/lab_host="BHB00 (harge=resistant)"
/note='Organ: skin; Vector: pcMV-SPORT6; Site_1: NotI;
Site_2: Sall; cloned unidirectionally. Primer: Oligo dr. Average insert size 2 kb. Library constructed by Life
                                                                                                                                                                          991 bp mRNA linear EST 05-FEB-2002
AGENCOURT_6475640 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5578048
5', mRNA sequence.
BM469251
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                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 991)
                                                                                                                                                                                                                                                                                                                                                                              NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammaiian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLML at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Matches 62
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KEYWORDS
SOURCE
ORGANISM
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BM468251
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ORIGIN
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AUTHORS
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JOURNAL
COMMENT
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Gaps

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1 cgcaggcagaccatgtggaccctg 										1 aacagggcagtggccttgtccagctcg
Ń	61	121	181	241	301	361	421	481 534	541	601
Qy Db	Oy Pp	Q Pp	Qy Dp	OY Ob	Qy Db	Oy Dp	Qy Dp	93 Pb	OY Dp	Oy Db

Search completed: September 5, 2002, 15:34:05 Job time: 8743 sec

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Sequence 73, Sequence 5, A Sequence 1, A

Sequence 1, Appli Sequence 1, Appli Sequence 18, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli

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GENERAL INFORMATION:
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL SETTLEO, GINETTE
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 2996.488/P001-A
CURRENT APPLICATION NUMBER: US/08/991,862
CURRENT FILING DATE: 1998-08-17
EARLIER FILING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PATENTIN VET: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: CDS
LOCATION: (13)..(1791)
COTER INFORMATION: Nucleotide sequence of human granulin/epithelin
OTHER INFORMATION: precursor (human GP88). Human Granulin Genebank
OTHER INFORMATION: M75161.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-07-668-648-3
Sequence 3, Application US/07668648
Sequence 3, Application US/07668648
Sequence 3, Application US/07668648
GENERAL INFORMATION:
APPLICANT: Shoyab, Mohammed
APPLICANT: Plowman, Gregory D.
TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
TITLE OF INVENTION: MODULATING PROTEINS
NUMBER OF SEQUENCE: 12
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 60; DB 4; I
Best Local Similarity 100.0%; Pred. No. 2.3e-12;
Matches 60; Conservative 0; Mismatches 0;
US-08-457-646A-6
US-08-45-076A-6
US-08-45-233A-4
US-08-74-5335A-6
US-08-74-56
US-08-729-214-6
US-09-729-334-1
US-08-90-823-73
US-08-90-823-73
US-08-394-189B-1
US-08-36-704-1
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US-08-508-004<sup>3</sup>
US-08-402-066-3
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: 1155 Avenue of the Americas
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-991-862-16
; Sequence 16, Application US/08991862
; Patent No. 6309826
                                                      28958
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LENGTH: 2095
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          TYPE: DNA
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131.919 Million cell updates/sec
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
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/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
                                       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-429-998-3
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US-08-429-998-7
US-08-421-33-7
US-08-421-33-7
US-08-421-33-7
US-08-421-33-7
US-08-421-33-5
US-08-991-862-1
US-08-991-862-1
US-08-991-862-1
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US-08-91-998-1
US-08-91-0321-1
US-08-429-998-1
US-08-421-33-1
US-08-421-1
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US-08-421-1
US-08-446-549-1
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                          nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq length: 0
seq length: 2000000000
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Match Length
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Perfect score:
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Gaps

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Length 2095; Indels

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ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: PREADIN FOLDOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/431,333
FTLING DATE: 27-APR-1995
FTLING DATE: 27-APR-1995
FTLING DATE: 27-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 58.4; DB 2;
Pred. No. 8.2e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 27-APR-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/668,648
FILING DATE: 13-MAR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/08431333 Patent No. 5965723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Plowman, Gregory D.
TITLE OF INVENTION: EPITHELINS:
TITLE OF INVENTION: MODULATING INTERES OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
                   REFERENCE/DOCKET NUMBER: 562
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)790-9090
TELEFAX: (212) 869-9741
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1779 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPPLOCY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                             \97.3%;
98.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,8
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                           MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
ORGANISM: Homo saptens
TISSUE TYPE: Kidney
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 98.3
Matches 59; Conservative
    REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                           11:1779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: New York STATE: New York
                                                                                                                                                                                                                                                                                                                                                        LOCATION:
US-08-429-998-3
                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Shoyab, Mohammed
APPLICANT: Plowman, Gregory D.
TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
TITLE OF INVENTION: MODULATING PROFEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     i; Indels
                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/668,648 FILING DATE: 19910819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/429,998
FILING DATE: 27-APR-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 58.4; DB 1;
Pred. No. 8.2e-12;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PILING DATE: 27-APR-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/668,648
FILING DATE: 13-MAR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/08429998 Patent No. 5885961
                                                                                                                                                                                                     ATTORNET/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,824
REFERENCE/COCKET NUMBER: 5624
TELECOMUNICATION INFORMATION:
TELERAN: (212) 869-9741
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1779 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 97.3%;
Best Local Similarity 98.3%;
Matches 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapien
TISSUE TYPE: Kidney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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: USA
                                                                                                                                                                  FILING DATE: 19
CLASSIFICATION:
10036
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LOCATION:
US-07-668-648-3
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                                                                                                                                                                                                                97.3%; Score 58.4; DB 2; Length 1779; 98.3%; Pred. No. 8.2e-12; Live 0; Mismatches 1; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application PC/TUS9102321
GENERAL INFORMATION:
APPLICANT: Shoyab, Mohammed
APPLICANT: Plowman, Gregory D.
TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
TITLE OF INVENTION: MODULATING PROTEINS
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
WEDIOM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/02321
FILING DATE: 19910403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Bristol-Myers Squibb Company 3005 First Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 0N0071A-PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)728-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: POOT, Brian W.
REGISTRATION NUMBER: 32,928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (206)448-4775
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1779 base pairs
TYPE: NUCLEIC ACID
                    MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSUE TYPE: Kidney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
TISSUE TYPE: Kidney
                                                                                                                                                                                                                                                         59; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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STATE: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: CDNA ORIGINAL SOURCE:
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TOPOLOGY: linear
                                                                                                                                                                                                                              Best Local Similarity
Matches 59; Conserv
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STREET: 300
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TELEFAX: (
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                                                                                                                                  ; LOCATION:
US-08-431-333-3
                                                                                                                    NAME/KEY:
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PCT-US91-02321-3
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Score 34.4; DB 1; Length 539;
Pred. No. 0.0015;
0; Mismatches 6; Indels
                                                                                                                                                                      Gregory D.
EPITHELINS: NOVEL CYSTEINE-RICH GROWTH MODULATING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gregory D. EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
                                                                                                                                                                                                                                                                                                                                                                                                                       SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MODULATING PROTEINS
                                                                                                                                                                                                                                                             ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/668,648
FILING DATE: 19910819
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Patent No. 5885961
GENERAL INFORMATION:
APPLICANT: Shoyab, Mohammed
APPLICANT: Plowman, Gregory D.
                                                                                                   Sequence 7, Application US/07668648
Patent No. 5416192
                                                                                                                                                                                                                                                                                                                                                                                                       IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: MISTOCK, S. LESIIE
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 56
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)790-9090
                                                                                                                                                         Mohammed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 57.3%;
Best Local Similarity 85.0%;
Matches 51; Conservative
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NAME: Misrock, S. Leslie
                                                                                                                                                                                                                                                                                                                                               ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Flòppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (212) 869-9741
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 539 base pairs
NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE TYPE: Kidney
                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Shoyab, N
APPLICANT: Plowman,
                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                               CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 199
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: line
MOLECULE TYPE: C
ORIGINAL SOURCE:
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US-07-668-648-7
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27-APR-1995
N: 536
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Best Local Similarity 85.0%;
Matches 51; Conservative
                                                                                                                                                                                                                                                      TELEPHONE: (212)790-9090
TELEFAX: (212) 869-9741
INFORMATION FOR SEQ ID NO: 7
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 539 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Bos taurus
TISSUE TYPE: Kidhey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Seattle
STATE: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
LOCATION: 1..537
                                                                         CLASSIFICATION:
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PCT-US91-02321-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Shoyab, Mohammed
APPLICANT: PLOWMAN, Gregory D.
TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
TITLE OF INVENTION: MODULATING PROTEINS
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/429,998
FILING DATE: 27-APR-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/668,648
FILING DATE: 13-WAR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                    1155 Avenue of the Americas
                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                               NAME: MISTOCK, S. LESIIE
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)799-9090
TELEPHONE: (212)799-9741
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                     Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 539 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE TYPE: Kidney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: CDNA ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM:
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Best Local Similarity
Matches 51; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                       New York
: New York
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                                                                                                                                10036
                                 ADDRESSEE:
STREET: 13
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103 TCCAAGGAGAACGCT---ACGGACCTCCTCACCAAGCAGCACACACACACACACGGGAT 159
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GENERAL INFORMATION:
APPLICANT: Shoyab, Mohammed
APPLICANT: Plowman, Gregory D.
TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
TITLE OF INVENTION: MODULATING PROTEINS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bristol-Myers Squibb Company
STREET: 3005 First Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 34.4; DB 2; Length 5 Pred. No. 0.0015; 0; Mismatches 6; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/02321
FILING DATE: 19910403
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 32,928
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/668,648
FILING DATE: 13-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624-161-99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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1;

Gaps

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13; Indels

0; Mismatches

Conservative

39;

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Matches
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Pred. No. 0.0015;
0; Mismatches 6; Indels
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MEDIUM TYPE: Floppy disk
CONFUTER: IBM PC compatible
OPFRATING SYSTEM: PC-DOS/MS-DOS
SOFWARRE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: US/07/668,648
FLILIG DATE: 19910819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                 US-07-668-648-5; Sequence 5, Application US/07668648; Sequence 5, Application US/07668648; Patent No. 5416192; GENERAL INFORMATION:
APPLICANT: Shoyab, Mohammed
APPLICANT: Plowman, Gregory D.; TITLE OF INVENTION: EPITHELINS: NC. TITLE OF INVENTION: MOULATING PR. NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624
TELEPHONE: (212)790-9090
SEQUENCE CHARACTERISTICS:
LENGTH: 1767 base pairs
                                                                                                                                                                                                                                               57.3%;
85.0%;
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MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                    Conservative
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                       ORGANISM: Bos taurus
TISSUE TYPE: Kidney
FEATURE:
   NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Mus muscu
TISSUE TYPE: Kidney
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                                                          MOLECULE TYPE: CDNA ORIGINAL SOURCE:
                                        linear
                                                                                                                                                                         1..537
                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 51; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY: CDS
; LOCATION: 1..1
US-07-668-648-5
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   TYPE: NUCLEIC STRANDEDNESS:
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                                                                                                                                                    ; NAME/KEY:
; LOCATION:
PCT-US91-02321-7
                                        TOPOLOGY:
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                                                                                                                                                                                                                                                   Query Match
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Score 31.2; DB 1; Length 1767; Pred. No. 0.021;

52.0%; 75.0%;

Query Match Best Local Similarity

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8 agaacgetaccacggacetecteactaagetgeetgegeacacagtgggega 59
                                                                                                                                                                                                                Gregory D. EPITHELINS: NOVEL CYSTEINE-RICH GROWTH MODULATING PROTEINS
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CURRENT APPLICATION DATA:
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Pred. No. 0.021;
0; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/668,648
FILING DATE: 13 MAR-1991
ATORNEY/AGENT INFORMATION:
NAME: MISTOCK, S. Leslie
REGISTRATION NUMBER: 18,872
REFERNICE/DOCKET NUMBER: 5624-161-99
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)790-9990
                                                                                                                                                                                                                                                                                                                      E: Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/429,998
FILING DATE: 27-APR-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: Ploppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS OSTWARE: PatentIn Pales
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US-08-431-333-5
; Sequence 5, Application US/08431333
; Patent No. 5965723
; GENERAL INFORMATION:
                                                                                                                       US-08-429-998-5; Sequence 5; Application US/08429998; Patent No. 5885961; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 52.0%;
Best Local Similarity 75.0%;
Matches 39; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (212)790-9090
TELEFAX: (212) 869-9741
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHRACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1767 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 1:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & 1
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TISSUE TYPE: Kidney
                                                                                                                                                                                                    APPLICANT: Shoyab, MC
APPLICANT: Plowman, G
TITLE OF INVENTION: F
TITLE OF INVENTION: N
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                                                                                                                                                                                                                                                                                                                                                             CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; NAME/KEY:
; LOCATION:
US-08-429-998-5
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LOCATION: (23)..(1789)
CTHER INFORMATION: The sequence is identical to that of the published
CTHER INFORMATION: mouse granulin except for one nucleotide (T
OTHER INFORMATION: instead of G) at position 1071 of GP88 cDNA
CTHER INFORMATION: (position 1056 of mouse granulin).
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APPLICANT: SETTETC, GLOETTE
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 29996.48FP001-A
CURRENT APPLICATION NUMBER: 0S/08/991,862
CURRENT FILING DATE: 1998-08-17
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Pred. No. 0.021;
0; Mismatches 13; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 31.2; DB 5; Length 1. Pred. No. 0.021; 0; Mismatches 13; Indels
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNBER: PCT/US91/02321
FILING DATE: 19910403
CLASSIFICATION: 514
ATTORNEY/ACTER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EARLIER APPLICATION NUMBER: 08/863,862
EARLIER FILING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 2137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Mouse epithelin/granulin
                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: POOL' BIJAN W
REGISTRATION NUMBER: 32,928
REFRENCE/DOCKET NUMBER: ONOO'
TELECOMMUNICATION INFORMATION:
TELEFONE: (206)728-4800
TELEFAX: (206)448-4775
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08991862 Patent No. 6309826
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Best Local Similarity 75.0%;
Matches 39; Conservative
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Best Local Similarity 75.0%;
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1767 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE TYPE: Kidney
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; LOCATION:
PCT-US91-02321-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
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Pred. No. 0.021;
0; Mismatches 13; Indels 0
                                                                                        APPLICANT: Plowman, Gregory D.
FITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
FITLE OF INVENTION: MODULATING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application PC/TUS9102321
GENERAL INFORMATION:
APPLICANT: Shoyab, Mohammed
APPLICANT: Plowman, Gregory D.
TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
TITLE OF INVENTION: MODULATING PROTEINS
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 agaacgetaccacggacetecteactaagetgeetgegeacacagtgggega
                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/431,333
FILING DATE: 17-APR-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/668,648
FILING DATE: 13-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: MISTOCK, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624-161-999
TELECOMMUNICATION INFORMATION:
METERENCE/DOCKET NUMBER: 5624-161-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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STREET: 3005 First Avenue
                                                                                                                                                                                                                 STREET: 1155 Avenue of the Americas CITY: New York
                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                      NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52.0%;
75.0%;
                                                                    Shoyab, Mohammed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (212)790-9090
TELEPAX: (212) 869-9741
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1767 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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1..1767
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Matches 39; Conserve
                                                                                                                                                                                                                                                                New York
: USA
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                                                                                                                                                                                                                                                                                                         10036
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LOCATION:
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Gaps

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RESULT 15

WESULT 15
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Query Match
44.0%; Score 26.4; DB 1; Length 1767;
Best Local Similarity 69.2%; Pred. No. 0.96;
Matches 36; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
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Search completed: September 5, 2002, 18:22:14 Job time: 13337 sec

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September 5, 2002, 18:30:01 ; Search time 457.59 Seconds
(without alignments)
225.125 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                  1 tecaaggagaacgetaceac......tgcgcacacagtgggcgat 60
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/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /SIDS5/gcgdata/geneseq/geneseqn-embl/NR1983.DAT:/SIDS5/gcgdata/geneseq/geneseqn-embl/NR1984.DAT:/SIDS5/gcgdata/geneseq/geneseqn-embl/NR1985.DAT:/SIDS5/gcgdata/geneseq/geneseqn-embl/NR1986.DAT:/SIDS5/gcgdata/geneseq/geneseqn-embl/NR1986.DAT:/SIDS5/gcgdata/geneseq/geneseqn-embl/NR1987.DAT:/SIDS5/gcgdata/geneseq/geneseqn-embl/NR1988.DAT:/SIDS5/gcgdata/geneseq/geneseqn-embl/NR1988.DAT:/SIDS5/gcgdata/geneseq/geneseqn-embl/NR1988.DAT:/
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/SIDS5/gcgdata/geneseq/geneseqn-embl/NA1981.DAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3472872
GenCore version 4.5
Copyright (c) 1993 - 2000 -Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1736436 seqs, 858457221 residues
                                                                                                                                                                                                                                                                      US-09-824-647-16_COPX_796_855
60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                             OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 200000000
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Match Length DB
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                                                                                                                                                                                                                                                                                                                       Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                         Scoring table:
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                                                                                                                                                                                                                                                                                                                                                  Sequence:
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                                                                                                                                                                       Run on:
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                                                                                                                                                                                                                                                                                           Title:
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	10	31.2	52.0	2137	20	AAV82824		Mouse GP88 autocri
	11	26.4	44.0	1767	12	AAQ14338		
	12	24.6	41.0	423	22	ABA44981		
	13	24.6	41.0	423	22	ABA55457		
	14	24.6	41.0	423	22	ABA25175		Probe #3641 for ge
	15	24.6	41.0	423	22	AAK03696		Human brain expres
	16	24.6	41.0	423	22	AAK29156		
	17	24.6	41.0	423	22	AAI13744		Probe##3677 for ge
	18	24.6	,41.0	423	22	AAI35104		Probe #3790 used t
	19	24.6	41.0	423	22	AAI03625		Probe #3616 used t
ပ	20		41.0	3512	20	AAV69395		H. contortus PGP-0
	21	24.4	40.7	100	17	AAT30909		Primer F5 for 80 k
Ç	22	◂	40.7	1377	22	AAI70511	_	Rice tryptophan de
	23	4	40.7	2203	17	AAT30869		Engineered 80 kD p
	24	23.8	39.7	1909	21	AAC49855		Arabidopsis thalia
	25	23.4	39.0	159	22	ABA70391		Human foetal liver
	26	23.4	39.0	159	22	AAK18628	(÷	Human brain expres
	27	23.4	39.0	159	22	AAK44555		Human bone marrow
	28	23.4	39.0	159	22	AAI50540		Probe #19226 used
	29	23.4	39.0	441	23	AAS69469		DNA encoding novel
ပ	30	23.4	39.0	447	23	AAS69468		
	31	23.4	39.0	488	22	ABA57774		Human foetal liver
	32	23.4	39.0	× 488	22	AAK05839		Human brain expres
	33	23.4	39.0	488	22	AAK31472		Human bone marrow
	34	23.4	39.0	488	22	AA137357		Probe #6043 used t
	35	23.4	39.0	563	22	AAS05614		Mammalian vestibul
	36	23.4	39.0	1550	21	AAC76777		Human ORFX ORF2332
	37	23.4	39.0	1553	22	AAH13982		Human cDNA sequenc
O	38	23.4	39.0	1642	22	AAD08067		Human SPOP TRAF-pr
υ	39	23.4	39.0	1642	22	AAH02922		Human shear stress
υ	40	23.4	39.0	2012	24	AAS18136		Human DNAX cytokin
	41	23.4	39.0	2141	23	AAS72373		DNA encoding novel
U	42	23.4	39.0	2789	21	AAF18162		Lung cancer associ
	43	23.4	39.0	3978	23	ABL14929		Drosophila melanog
	44	23.4	39.0	4181	13	AAQ29345		MCC gene of chromo
Ó	45	23.4	39.0	6557	23	ABL14928		Drosophila melanog
						ALIGNMENTS	NTS	•

ALIGNMENTS

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GP88; granulin; epithilin; human; growth factor; autocrine; tumour;
cancer; viral infection; antagonist; therapy; diagnosis; ss.
                                                                                                                                  Human GP88 autocrine growth factor cDNA.
                                                                                                                                                                                                                                                  Location/Qualiflers
13..1794
/*tag= a
                                 AAV82825 standard; cDNA; 2095 BP
                                                                                                                                                                                                                                                                                                                                                                                                                         970S-0991862.
970S-0863079.
                                                                                                                                                                                                                                                                                                                                                                                          98WO-US10555
                                                                                                  (first entry)
                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                         WO9852607-A1
                                                                                                                                                                                                                                                                                                                                                                                                                         16-DEC-1997;
23-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                          22-MAY-1998;
                                                                                                15-MAR-1999
                                                                                                                                                                                                                                                                                                                                                          26-NOV-1998
                                                                  AAV82825;
RESULT
AAV82825
                                                                                                                                                                                                                                                       Key
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(SERR/) SERRERO G.

Granulin coding se Granulin coding se Human cDNA clone (Human cDNA sequenc

> AAQ49052 AAH07141 AAH16370 AAQ14339

> > 58.4 58.4 58.4 34.4

Human epithelin pr Human cancer assoc Bovine epithelin p Mouse epithelin pr

Serrero G;

Gaps

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Indels

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Length 2124;

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1 tecaaggagaaakegetaccacggacetecteactaagetgeetgegeacacagtgggegat 60
                                                                                                                                                                      The granulin inhibits keratinocytes and is useful in formulations
                                                                          New cystine rich granulin peptide(s) from leucocyte(s) - are keratinocyte inhibitors useful topically for wound healing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Granulin; keratinocytes; wound healing; inhibition; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New cystine rich granulin peptide(s) from leucocyte(s) – a)
keratinocyte inhibitors useful topically for wound healing
                                                                                                                                                                                                                             Sequence 2124 BP; 383 A; 685 C; 630 G; 426 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2198 BP; 398 A; 708 C; 646 G; 446 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /transl_except= CAG encodes Glycine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= a
/transl_except= ATG encodes Valine.
1714..1716
                                                                                                                                                                                                                                                                                   100.0%; Score 60; DB 14;
100.0%; Pred. No. 2:2e-12;
                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The granulin inhibits keratinocytes and for promoting the healing of wounds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Figure 4c; 53pp; English
                                                                                                                                     Disclosure; Figure 4c; 53pp; English
                                                                                                                                                                                         for promoting the healing of wounds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
1453..1455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAQ49052 standard; DNA; 2198 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 granulocytes; leucocytes; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92US-0829233.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Granulin coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag-
                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1993-320328/40.
P-PSDB; AAR48673.
                     WPI; 1993-320328/40.
                                         P-PSDB; AAR48673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-FEB-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-FEB-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            409315195-A
                                                                                                                                                                                                                                                                                                                           90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Solomon S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAQ49052;
                                                                                                                                                                                                                                                                                                                                                                                                   809
                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                   Op
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                  This human cDNA sequence includes a coding region for GPBB (see AAMB5474), an BB kDa glycoprotein autocrine growth factor and epithilin/granulin precursor that is expressed in a tightly regulated manner in normal cells, is overexpressed and unregulated in highly tumorigenic cells derived from normal cells, and which cats as a stringently required growth stimulator for the tumorigenic cells. Inhibition of GPBB expression or action in the tumorigenic cells results in an inhibition of the tumorigenic properties of the overproducing cells. Antagonists to GPBB are used to raise specific antibodies (used as antagonists, GPBB are used to raise specific antibodies (used as antagonists, as diagnostic reagents and for delivering toxins or other compounds to GPBB-expressing cells) and to screen for antibodies. Antisense oligonucleotides can also be used as antagonists.

Methods are provided for diagnosing disease, or determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                        Composition containing antagonist of growth factor GPB8 - useful for treating cancer and viral diseases and also for diagnosing disease from altered GPB8 expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    susceptibility to disease, resulting from altered GP88 activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 2095;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  wound healing; inhibition; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2095 BP; 364 A; 681 C; 625 G; 425 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= a
/transl_except= ATG encodes Valine.
1640..1642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 100.0%; Score 60; DB 20; Best Local Similarity 100.0%; Pred. No. 2.2e-12; Matches 60; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                     Disclosure; Fig 9A; 86pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAQ56794 standard; DNA; 2124 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Granulin; keratinocytes; wour
granulocytes; leucocytes; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92WO-CA00089
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Granulin coding sequence
WPI; 1999-045276/04.
P-PSDB; AAW85475.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SOLO/) SOLOMON S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_difference
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is useful in formulations

03-FEB-1992;

Solomon S;

28-FEB-1992;

WO9315195-A. 05-AUG-1993

Homo sapiens

AAQ56794;

964

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ö
                        Gaps
                       ;
 Length 2198;
                        Indels
 Score 60; DB 14;
Pred. No. 2.2e-12;
Mismatches 0;
                       0; Mismatches
 ch 100.0%;
l Similarity 100.0%;
60; Conservative 0
Query Match
Best Local Similarity
                       Matches
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g à

AAH07141 standard; cDNA; 757 BP AAH07141 RESULT

AAH07141;

26-JUN-2001 (first entry)

Human cDNA clone (5'-primer) SEQ ID NO:3976.

Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.

EP1074617-A2.

07-FEB-2001

28-JUL-2000; 2000EP-0116126.

29-JUL-1999;

99JP-0300253. 2000JP-0118776. 11-JAN-2000; 7-AUG-1999;

2000JP-0183767. 2000JP-0241899. 02-MAY-2000; 09-JUN-2000;

HELI-) HELIX RES INST.

Yamamoto J; Saito K, Ya Otsuki T; A, Nagai K, Hayashi K, sogai T, Nishikawa T, Sugiyama T, Wakamatsu Isogai T, shii S,

WPI; 2001-318749/34.

Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the Full-length cDNAs

Claim 1; SEQ ID 3976; 2537pp + CD ROM; English.

The present invention describes primer sets for synthesising 5602 (ull-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligounclectide complementary to the complementary strand of a polynuclectide which comprises one of the 5602 nucleotide comprises at least 15 nucleotides, or (b) a combination of an oligonuclectide comprises a least 15 nucleotides; or (c) a combination of an oligonuclectide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonuclectide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence complementary to a polynucleotide which comprises a 3'-end sequence of sequence 3'-end sequence 3'-end sequence 1'-end detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to the present invention

Sequence 757 BP; 139 A; 232 C; 217 G; 165 T; 4 other;

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                                 Gaps
                 ;
 Length 757;
                 Indels
Score 58.4; DB 22
Pred. No. 7.2e-12;
0; Mismatches 1
 97.3%;
98.3%;
Query Match
Best Local Similarity 98.3
Matches 59; Conservative
                                     οy
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detection; diagnosis; antisense therapy; gene therapy; ss
                                                                                                                                                        Yamamoto J;
                                                      Human cDNA sequence SEQ ID NO:15309.
                        AAH16370 standard; cDNA; 1630
                                                                                                                      99JP-0300253.
2000JP-0118776.
                                                                                                       28-JUL-2000; 2000EP-0116126
                                                                                                                                    2000JP-0241899
                                                                                                                               2000JP-0183767
                                            (first entry)
                                                                                                                                              (HELI-) HELIX RES INST.
                                                                                                                     27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
                                                                           Homo sapiens
                                                                                    EP1074617-A2.
                                                                                                                 29-JUL-1999;
                                                                                                                                     09-JUN-2000;
                                            26-JUN-2001
                                                                                             07-FEB-2001
                                  AAH16370;
               2
                   AAH16370
               RESULT
q
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Saito K, Ya Otsuki T; Isogai T, Nishikawa T, Hayashi K, S. Sugiyama T, Wakamatsu A, Nagai K, Ishii S,

WPI; 2001-318749/34.

Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the Full-length cDNAs

Claim 8; SEQ ID 15309; 2537pp + CD ROM; English.

the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification The present invention describes primer sets for synthesising 5602 [411].length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5. end the full length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to the present invention

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ET-1 is a bifunctional growth regulator, capable of stimulating the growth of some cell types while inhibiting the growth of others. ET-2 is functionally similar to ET-1 w.r.t. growth inhibitory bloactivity. In contrast, however, ET-2 is apparently not capable of ellotting the growth stimulatory activity characteristic of ET-1 and, in fact, antagonises this ET-1 activity.

See also AAQ14338-40, AAQ14952-53, AAR14328-9 and AAR15315-20.
                                                                                                                                                                                                  ET-1 and ET-2 were isolated from rat kidneys and their amino acid sequences determined. A full length rat ET cDNA (AAQ14338) was obtd. by screening a rat kidney cDNA library in lambda gill with PCR generated ET probes. These probes were also used to obtain the mouse ET gene (AAQ14340) from a mouse T-cell genomic library ET DNA was also obtained from human sources (AAQ14339). An anti-sense ribonucleic acid molecule complementary to the indicated fragment in the features is also claimed
                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ET; anti-sense RNA; growth regulation; inhibition; stimulation; ss.
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                                                                                   Score 58.4; DB 22; Length 1630;
Pred. No. 8.2e-12;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New cysteine-rich growth modulating proteins, epithelins - us as inhibitors of neoplastic cell growth and to promote wound healing and treat psoriasis
Sequence 1630 BP; 285 A; 517 C; 489 G; 339 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41..1819
/*tag= a
/note= "claim 9, page 54"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 22; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                    AAQ14339 standard; DNA; 1779
                                                                                   97.3%;
98.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91US-0083796.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BRIM ) BRISTOL-MYERS SQUIB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91WO-0S02321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-JAN-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human epithelin precursor
                                                                                   Query Match 97.3°
Best Local Similarity 98.3°
Matches 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shoyab M, Plowman GD;
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P-PSDB; AAR14326.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-APR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-MAR-1991;
03-APR-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-0CT-1991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAQ14339;
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                                                                                                                                                                                                                                                                                                                                               RESULT
AAQ14339
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Sequence 1779 BP; 304 A; 578 C; 547 G; 350 T; 0 other;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polynucleotides, polypeptides, antibodies, agonists and antagonists from
the present invention may be used to treat immune disorders by activating
or inhibiting the proliferation, differentiation or mobilisation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAC77607 to AAC78448 encode the human cancer associated proteins given in AAB4339 to AAB44239. The proteins can have activities based on the tissues and cells the genes are expressed in. Example of activities include: cytostatic; proliferative; vulnerary; immunomodulator; antidabetic; antiasthmatic; antinheumatic; antiarthritic; antilnflammatory; antithyroid; antiallergic; antibacterial; antiviral; dermatological; neuroprotective; cardiant; thrombolytic; coaquiant; nootropic; vasotropic; antipsoriatic and antianglogenic. The polynucleotides and polypeptides can be used for preventing, treating or ameliorating medical conditions and diagnosing pathological conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         dermatological; neuroprotective; thrombolytic; coagulant; noctropic; vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation; immune disorder; haematopoletic cell disorder; autoimmune disorder; allergic reaction; graft versus host disease; organ rejection; haemostatic; thrombolytic; cardiovascular disorder; infection;
                                                                             diagnosis; cytostatic; proliferative; vulnerary; immunomodulator;
antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral;
antiinflammatory; antithyroid; antiallergic; antibacterial; cardiant;
                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immune cells, to treat disorders of haematopoietic cells, autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel isolated nucleic acids comprising sequences encoding peptides useful for treating or diagnosing e.g. cancer -
                                                                                                                                                                                                                                                                                                                                                                                  cancer associated gene; cancer antigen; detection; cancer;
                                         ö
Length 1779;
                                         Indels
                                                                                                                                                                                                                                                                                                                                          Human cancer associated gene sequence SEQ ID NO:574.
  Score 58.4; DB 12;
Pred. No. 8.3e-12;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 1097-1098; 2352pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neurological disease; drug screening; ss.
                                                                                                                                                                                                                AAC78180 standard; cDNA; 2432 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC.
  97.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0124270.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-MAR-2000; 2000WO-US05882
                                                                                                                                                                                                                                                                                                     (first entry)
                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-587533/55.
P-PSDB; AAB43971.
  Query Match
Best Local Similarity
Matches 59; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rosen CA, Ruben
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200055350-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                     08-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-SEP-2000
                                                                                                                                                                                                                                                             AAC78180;
                                                                                                                                                                                   RESULT
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ET; anti-sense RNA; growth regulation; inhibition; stimulation; ss.

36.

AAQ14340 standard; DNA; 1767 BP.

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RESULT

(first entry)

17-JAN-1992

AAQ14340;

Mouse epithelin precursor

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The epithelins appear to comprise several distinct members sharing significant structural homology. Two members of the epithelin family, EP-1 and EP-2, have been purified from natural sources, and cDNAs encoding these and several other members of the epithelin family have been isolated from rat (AAQ14338), human (AAQ14339), bovine, murine (AAQ14340) and chicken (AAQ14338), human (AAQ14339), bovine, murine ET-1 is a bifunctional growth regulator, capable of stimulating the growth of some cell types while inhibiting the growth of others. ET-2 is functionally similar to ET-1 w.r.t. growth inhibitors bloactivity. In contrast, however, ET-2 is apparently not capable of eliciting the growth stimulatory activity characteristic of ET-1 and,
                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New cysteine-rich growth modulating proteins, epithelins - useful as inhibitors of neoplastic cell growth and to promote wound healing and treat psoriasis
                                                                          ö
                                           Score 58.4; DB 21; Length 2432;
Pred. No. 8.7e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in fact, antagonises this ET-1 activity.
See also AAQ14338-40, AAQ14952-53, AAR14328-9 and AAR15315-20.
                                                                          Indels
Sequence 2432 BP; 460 A; 764 C; 707 G; 496 T; 5 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 539 BP; 99 A; 171 C; 163 G; 106 T; 0 other;
                                                                                                                                                                                                                                                                                                                                           ET; growth regulation; inhibition; stimulation; ss.
                                                                             ï
                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                              Bovine epithelin precursor (partial).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 24; 97pp; English.
                                                                                                                                                                                                                  BP.
                                           97.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91WO-US02321.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BRIM ) BRISTOL-MYERS SQUIB.
                                                                                                                                                                                                               AAQ14952 standard; DNA; 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 910S-0083796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 900S-0504508
                                                                                                                                                                                                                                                                            17-JAN-1992 (first entry)
                                                                          59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plowman GD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1991-325168/44.
                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; AAR15426.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-APR-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                      WO9115510-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                     17-0CT-1991
                                                                                                                                                                                                                                                                                                                                                                         Bos taurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shoyab M,
                                                                                                                                                                                                                                               AAQ14952;
                                           Query Match
                                                                          Matches
                                                                                                                                                                                                  AAQ14952
                                                                                                                                                                                    RESULT
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ET-1 and ET-2 were isolated from rat kidneys and their amino acid sequences determined. A full length rat ET cDNA (AAQ14318) was obtd. by screening a rat kidney cDNA library in lambda gil0 with PCR c generated ET probes. These probes were also used to obtain the mouse ET gene (AAQ14340) from a mouse T-cell genomic library. ET DNA was also obtained from human sources (AAQ14339).

ET DNA was also obtained from human sources (AAQ14339).

ET an anti-sense ribonucleic acid molecule complementary to the indicated fragment in the features is also claimed.

ET-1 is a bifunctional growth requiator, capable of stimulating the growth of some cell types while inhibiting the growth of others. C ET-2 is functionally similar to ET-1 w.r.t. growth inhibitory bloactivity. In contrast, however, ET-2 is apparently not capable of eliciting the growth stimulatory activity characteristic of ET-1 and, c in fact, antagonises this ET-1 activity.

See also AAQ14338-40, AAQ14952-53, AAR14328-9 and AAR15315-20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New cysteine-rich growth modulating proteins, epithelins - useful as inhibitors of neoplastic cell growth and to promote wound healing and treat psoriasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52.0%; Score 31.2; DB 12; Length 1767; llarity 75.0%; Pred. No. 0.064; Conservative 0; Mismatches 13; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1767 BP; 360 A; 503 C; 492 G; 412 T; 0 other;
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                                                                                                                                                                                     /*tag= a
/note= "claim 29, page 56"
                                                                                                                                                   Location/Qualifiers
8..1774
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                                                                                                                                                                                                                                                                                                                             910S-0083796.
                                                                                                                                                                                                                                                                                                                                                                            (BRIM ) BRISTOL-MYERS SQUIB.
                                                                                                                                                                                                                                                                                              91WO-US02321
                                                                                                                                                                                   /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                        Shoyab M, Plowman GD;
                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1991-325168/44.
P-PSDB; AAR14327.
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Best Local Similarity
Matches 39; Conserv
                                                                                                                         Mus musculus.
                                                                                                                                                                                                                                                                                                03-APR-1991;
                                                                                                                                                                                                                                                                                                                            13-MAR-1991;
03-APR-1990;
                                                                                                                                                                                                                                  WO9115510-A
                                                                                                                                                                                                                                                                 17-0CT-1991
                                                                                                                                                      Key
misc_RNA
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RESULT 10 AAV82824

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Gaps

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57.3%; Score 34.4; DB 12; Length 539; 85.0%; Pred. No. 0.0036; 1ive 0; Mismatches 6; Indels 3

Best Local Similarity 85.0 Matches 51; Conservative

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Query Match

807 agaactacaccacggatctcctgaccaagctgcctggatacccagtgaagga 858

11

RESULT

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This murine cDNA sequence includes a coding region for GPBB (see AAWB5474), an 88 kDa glycoprotein autocrine growth factor and compiling formula processed and unregulated regulated manner in normal cells, is overexpressed and unregulated in highly tumorigenic cells, is overexpressed and unregulated in highly tumorigenic cells derived from normal cells, and which carts as a stringently required growth stimulator for the tumorigenic cells. Inhibition of GPBB expression or action in the tumorigenic cells results in an inhibition of the tumorigenic cells results in an inhibition of the tumorigenic properties of the overproducing cells. Murine GPBB cDNA was isolated from the highly tumorigenic PC cell line CDNA library using a probe obtained by PCR using primers based on isolated GPBB peptides. Antagonists to GPBB are used to treat diseases associated with increased expression of GPBB, particularly cancer but also viral infections. Fragments of GPBB are used to raise specific antibodies (used as antagonists, as diagnostic reagents and for delivering toxins or other compounds to GPBB expressing cells) and to screen for antibodies. Antisense oligonucleotides can also be used as antagonists. Matchods are provided for delivering toxins or other compounds to disease, or determining susceptibility to disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       composition containing antagonist of growth factor GP88 - useful for treating cancer and viral diseases and also for diagnosing disease from altered GP88 expression
                                                                                                                                         GP88; granulin; epithilin; mouse; growth factor; autocrine; tumour; cancer; viral infection; antagonist; therapy; diagnosis; ss.
                                                                                                                                                                                                                                                                                                          /transl_except= (pos:182..184, aa:Asp)
/transl_except= (pos:1151..1153, aa:Cys)
/transl_except= (pos:1340..1342, aa:Leu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2137 BP; 443 A; 608 C; 583 G; 503 T; 0 other;
                                                                                                                                                                                                                                                                                           aa:Ile)
                                                                                                       Mouse GP88 autocrine growth factor cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from altered GP88 activity.
                                                                                                                                                                                                                                  Location/Qualifiers
23..1792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 5; Fig 8A-D; 86pp; English.
AAV82824 standard; cDNA; 2137 BP
                                                                                                                                                                                                                                                                                       /transl_except=/transl_except=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                98WO-US10555
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97US-0863079,
                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-045276/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SERR/) SERRERO G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; AAW85474
                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-MAY-1998;
                                                                    15-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                     W09852607-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-MAY-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Serrero G;
                                                                                                                                                                                                   Mus sp.
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sequences determined. A full length rat ET CDNA was obtd. by screening a rat kidney CDNA library in lambda gill with PCR generated ET probes. These probes were also used to obtain the mouse ET gene (AAQ14340) from a mouse T-cell genomic library. ET DNA was also obtained from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  An anti-sense ribonucleic acid molecule complementary to the indicated fragment in the features is also claimed.

ET-1 is a bifunctional growth regulator, capable of stimulating the growth of some cell types while inhibiting the growth of others.

ET-2 is functionally similar to ET-1 w.r.t. growth inhibitory bloactivity. In contrast, however, ET-2 is apparently not capable of eliciting the growth stimulatory activity characteristic of ET-1 and, in fact, antagonises this ET-1 activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                          ET; anti-sense RNA; growth regulation} inhibition; stimulation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New cysteine-rich growth modulating proteins, epithelins - useful as inhibitors of neoplastic cell growth and to promote wound healing and treat psoriasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ET-1 and ET-2 were isolated from rat kidneys and their amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1767;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          See also AAQ14338-40, AAQ14952-53, AAR14328-9 and AAR15315-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1767 BP; 359 A; 499 C; 491 G; 418 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 26.4; DB Pred. No. 3.6; 0; Mismatches
                                                                                                                                                                    سير.
                                                                                                                                                                                                                  /*tag= a
/note= "claim 19, page 55ª
                                                                                                                                                                                  Location/Qualifiers 31..1797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 18; 97pp; English.
             BP.
            AAQ14338 standard; cDNA; 1767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44.0%;
                                                                                                                                                                                                                                                                                                                                                  910S-0083796.
900S-0504508.
                                                                                                                                                                                                                                                                                                                      91WO-US02321.
                                                                                                                                                                                                                                                                                                                                                                                           (BRIM ) BRISTOL-MYERS SQUIB.
                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36; Conservative
                                                                                                Rat epithelih precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                         Shoyab M, Plowman GD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1991-325168/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sources (AAQ14339).
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAR14325
                                                                                                                                                           Rattus rattus
                                                                    17-JAN-1992
                                                                                                                                                                                                                                                                                                                      03-APR-1991;
                                                                                                                                                                                                                                                                                                                                                  13-MAR-1991;
                                                                                                                                                                                                                                                                                                                                                                 03-APR-1990;
                                                                                                                                                                                                                                                               WO9115510-A.
                                                                                                                                                                                                                                                                                         17-0CT-1991
                                          AAQ14338;
                                                                                                                                                                                                    misc_RNA
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AAQ14338
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Gaps

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Indels

13;

0; Mismatches

39; Conservative

Best Local Similarity Matches 39; Conserv

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Query Match

52.0%; Score 31.2; DB 20; Length 2137; 75.0%; Pred. No. 0.066;

8 agaacgctaccacggacctcctcactaagctgcctgcgcacacagtgggcga 59

12

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Human; foetal liver; gene expression; single exon nucleic acid probe; ss.

liver single exon nucleic acid probe #3762.

Human foetal

(first entry)

01-FEB-2002

ABA55457;

ABA55457 standard; DNA; 423 BP.

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nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 414 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less bias
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a spatially-addressable set of single exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes -
                                                                                                                                                                             Human; microarray; single exon probe; gene expression; breast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 3676; 327pp + sequence listing; English.
                                                                                                                                  Human breast cell single exon nucleic acid probe #3676.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 423 BP; 110 A; 126 C; 100 G; 87 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 24.6; DB
Pred. No. 13;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chen W, Rank DR;
                    ABA44981 standard; DNA; 423 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MOLE-) MOLECULAR DYNAMICS INC
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llarity 70.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0632366.
2000US-0234687.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0608408
                                                                                                                                                                                                                                                                                                                                                       30-JAN-2001; 2001WO-US00662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000GB-0024263
                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hanzel DK,
                                                                                                                                                                                                  disease; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-496933/54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 33; Conserv
                                                                                                                                                                                                                                                                           WO200157271-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                           04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-OCT-2000;
                                                                                             01-FEB-2002
                                                                                                                                                                                                                                                                                                                  09-AUG-2001
                                                           ABA44981;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Penn SG,
ABA44981
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Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver -

Rank DR;

Chen W,

Hanzel DK,

Penn SG,

WPI; 2001-483447/52.

(MOLE-) MOLECULAR DYNAMICS INC

20000S-0207456. 20000S-0608408. 20000S-0632366.

26-MAY-2000; 30-JUN-2000; 03-AUG-2000;

2000US-0234687 2000US-0236359 2000GB-0024263

21-SEP-2000; 27-SEP-2000; 04-OCT-2000;

2000US-0180312

04-FEB-2000;

30-JAN-2001; 2001WO-US00669

WO200157277-A2.

09-AUG-2001.

Homo sapiens,

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                                      The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Probe #3641 for gene expression analysis in human heart cell sample.
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                                                                                                                                                                                                                                                                                                                                                 Length 423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; gene expression; heart; microarray; vascular system; cardiovascular disease; hypertension; cardiac arrhythmia; congenital heart disease; ss.
Claim 1; SEQ ID NO 3762; 639pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 423 BP; 110 A; 126 C; 100 G; 87 T; 0 other;
                                                                                                                                                                                                                                                                                                                                            Query Match 41.0%; Score 24.6; DB 22; Best Local Similarity 70.2%; Pred. No. 13; Matches 33; Conservative 0; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP.
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Gaps

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à g RESULT 13 ABA55457

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                                                                                                                                                                                                                                                                                                                The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
                                                                                                                                                                                                                                                                                                                                                                                                                     Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                        Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human brain expressed single exon probe SEQ ID NO: 3687.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 423 BP; 110 A; 126 C; 100 G; 87 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 13;
0; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 24.6;
                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID No 3641; 530pp; English.
                                                                                                                                                                                                            Rank DR;
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                                                                                                                                                                                   (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                          Chen W,
                                                                                                   26-MAY-2000; 20000S-0207456.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0235399.
04-OCT-2000; 2000GB-0024263.
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                                                                  30-JAN-2001; 2001WO-US00666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 41.0
Best Local Similarity 70.2
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            congenital heart disease.
                                                                                                                                                                                                          Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   epilepsy; cancer; ss
                                                                                                                                                                                                                                 WPI; 2001-488899/53
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                     WO200157274-A2
  Homo sapiens.
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                                                                                         04-FEB-2000;
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                                             09-AUG-2001
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                                                                                                                                                                                                          Penn SG,
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The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple scherosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                                                                                              Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 4; SEQ ID NO: 3687; 650pp + Sequence Listing; English.
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Pred. No. 13;
0; Mismatches 14; Indels 0;
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                                                                                                                                                                                                                                                          Rank DR;
                                                                                                                                                                                                    (MOLE-) MOLÈCULAR DYNAMICS INC
                                                                                                                                                                                                                                                          Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41.0%;
                                                                           03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-02635959.
04-OCT-2000; 2000GB-0024263.
2000US-0180312
                             2000US-0207456
                                                   2000US-0608408
                                                                        2000US-0632366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 41.0
Best Local Similarity 70.2
Matches 33; Conservative
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Job time: 10534 sec
                                                                                                                                                                                                                                                          Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                                                                           WPI; 2001-483446/52
04-FEB-2000;
26-MAY-2000;
                                                   30-JUN-2000;
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BE741541 601594837 BIRB35123 603087789 BC423187 602450504 BW043523 603519942 BE742649 601575484 AU135509 AU135509 BE742649 601575484 BE743649 7 60276935 BE748277 602769335 BE407219 601301331 BE258826 601117359 BH198717 602759720 BH198717 602759720 BH198712 602750013 BW048423 60356013 BE968260 60226903 AU134038 AU134038 BE325407 602953251 BE325407 602953251 BE325407 602953251 BE36839 601277948 BE407885 601297948 BE407885 601297948 BE345137 602108313 BC348475 602409109 BW04588 602409109 BW04588 602409109

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BE741541 B1835123 B1835123 B0A23187 B0A3523 B0A43523 B0A43529 B0A43509 B1336895 B136826 B1368423 BMO48423 BMO48423 BMO48423 B1193612 BMO48423 BF968260 A1134038 B1252407 B2366839 B1252407 B286839 B1252407 B286839 B1252407 B286839 B1252407 B286839 B1252407 B286839 B1252407 B1252407 B1252407 B1252407 B1252407 B12528485 B18773396 B18773396

AL551474 AL551474

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A1751894 cn12e0.x.
BF99853 CM2-GN016
BG015966 RC4-GN032
BF998626 CM2-GN016
BG014975 RC4-GN032
BE970308 G0148765
BF970308 G02273694
AW579074 RC0-CT038
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AA122084 zm23e01.r
BF925544 CM2-NT016
BG004140 CM2-GN016
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BI159891 602863719
BE253430 601111692
BE302516 ba66903.y
                                                    5, 2002, 15:34:05; Search time 3259.55 Seconds (without alignments) 248.445 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                                                            27472414
               Compugen Ltd.
                                                                                                                                           13736207 segs, 6748477542 residues
                                                                                                                                                          Total number of hits satisfying chosen parameters:
      GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
                                                                                    US-09-824-647-16_COPY_796_855
                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                      nucleic search, using sw model
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BF018965
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Gapop 10.0 , Gapext 1.0
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gb_estl:*
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Maximum DB seq length: 2000000000
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Match Length
                                                     September
                                                                                                                                                                                                                                   EST:*
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Perfect score:
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                                     OM nucleic
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ALIGNMENTS	AW062972 134 bp mRNA linear EST 06-OCT-1999 ILL-ST0041-020899-001-F07 ST0041 Homo saplens cDNA, mRNA sequence. AW062972 GI:6014357 EST. EST. Human saplens cDNA, mRNA sequence bunnary saplens cDNA, mRNA sequence. AW062972.1 GI:6014357 EST.		as as as equ :/w //w Lme Lme	Location/Qualifiers 1134 /organism="Homo sapiens" /ob_xref="taxon:9606" /db_xref="taxon:9606" /db_xrege="Adult" /dev_stage="Adult" /note="Organ: stomach; Vector: pGC18; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORSTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research)
	RESULT 1 AW062972/C LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ODGENISM	REFERENCE AUTHORS TITLE JOURNAL COMMENT		FEATURES SOUTCE

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Contact: Wilson RK
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                                                                                                                                                                                                                        mRNA sequence.
AA122084
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                 human.
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                                                                                                                                                                                    DEFINITION
                                                                                                                                                                                                                                                                                                                                  ORGANISM
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    of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: asimpsoneludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtmi2.pl?tl=RC4&t2=RC4-MT0235-131200-021-b04&t3=2000-12-13&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 52
High quality sequence start: 52
High quality sequence start: 54
                                                                                                                                                                                                                                                                                                                                                                        BF902443 . 369 bp mRNA linear EST 18-JAN-2001 RC4-MT0235-131200-021-b04 MT0235 Homo sapiens cDNA, mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 369)
profiles into the pUC 18 vector. Reverse transcription tissue mRNA and cDNA amplification were performed under low stringency conditions.
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Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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20202663
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Pred. No. 3.8e-09;
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/db_xref="taxon:9606"
/clone_lib="MT0235"
/dev_stage="Adult"
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                                                                                                                                            ch 97.3%;
1 Similarity 98.3%;
59; Conservative
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| 1. .393 | Arganism=Homo sapiens | Arganism=Homo sapiens | Arganism=Homo sapiens | Arzef="EdbB:3917917" | Ab_xref="EdbB:3917917" | Ab_xref="EdbB:3917917" | Ab_xref="Stragene pancreas (#937208) | Arganism=Stragene pancreas (#937208) | Arganism=Stragene pancreas; Vector: palluescript SK-; Site_1: Anoi; Anoi; Arganism=Stragene | Arganism=Stragene
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EST 23-DEC-1997
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                                              AA122084 15 13-DEC-199 2m23e01.rl Stratagene pancreas (#937208) Homo sapiens CDNA clone INAGE:526488 5' similar to gb:X62320 GRANULINS PRECURSOR (HUMAN);,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: estewatson.wustl.edu
WARNING: There is evidence that suggests that the 384-well parent
plate of this clone contains both human and mouse derived clones.
Thus, the origin of this clone is uncertain. This caution should kept in mind should you use this clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1145 Std Error: 0.00 Seq primer: -28M13 rev2 from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Pred. No. 5.3e-09;
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Indels

Length 369;

Score 58.4; DB 10; Pred. No. 5.2e-09;

Query Match 97.3%; Best Local Similarity 98.3%; Matches 59; Conservative

0; Mismatches

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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1 (bases 1 to 394)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
'M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Pred. No. 5.3e-09;
0; Mismatches 1;
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AUTHORS
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                                                                    BF925544 1100-525-c04 NT0169 Homo sapiens CDNA, mRNA sequence.
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl-cM2&t2=CM2.NT0169-
291100-525-c04&t3=2000-11-29&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 17
High quality sequence stop: 394.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                           Homo sapiens
Mukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 394)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shotgun sequencing of the human transcriptome with ORF expressed
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Pred. No. 5.3e-09;
0; Mismatches 1; Indels 0;
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/db_xref="taxon:9606"
/clone_lib="NT0169"
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BF925544.1 GI:12321984
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Length 394; Indels

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СМ2-GN0166-101100-496-f05 GN0166 Homo sapiens CDNA, mRNA sequence.
BF998533
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1 (bases 1 to 457)
10 also Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matshkuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CMZet2=CM2-GN0166-101100-496-f056t3=2000-11-106t4=1)
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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                                                                                             Health
10/10C101, 9000 Rockville Pike, Bethesda, MD 20892-1267,
Tel: 301-402-4877
                                                                                                                                                                                                                                                                                                    /clone_lib="Normal Human Trabecular Bone Cells"
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                                                                Email: libin@helix.nih.gov

DNA Sequencing and analyses by National Institutes of Intramural Sequencing Center (NISC).

Plate: 12 row: e column: 02

Seq primer: -21M13 forward primer (ABI).

Location/Qualifiers
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20202663
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                                                                                                                                                                                                                                                                                                                                               /tissue_type="Bone"
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/lab_host="SURE"
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Pred. No. 5.5e-09;
0; Mismatches 1;
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/db_xref="taxon:9606"
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/db_xref="taxon:9606"
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High quality sequence stop: 328
Location/Qualifiers
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1 Similarity 98.3%;
59; Conservative
                                             Fax: 301-496-7157
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BF998533/c
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/note="Organ: placenta_normal; Vector: puc18; Site_1: Smal : Site_2: Smal; A mini-library was made by cloning products derived from ORESTES CR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 460)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,

Nagai,M.A., da Silva,W. Jr., Zago,M.A., Badin,S., Costa,F.F.,

Goldman,G.H., Carvalho,A.F.; Matsukuma,A., Baia,G.S., Simpson,D.H.,

Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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Fax: +55-11-2707001
Enail: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl7tl=RC4&t2-RC4-GN0323-281200-032-901&t3-2000-12-28&t4-1)
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          \operatorname{Simpson}, A.\mathsf{J} . Shotgun sequencing of the human transcriptome with ORF expressed Shotgun
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1jarity 98.3%; Pred. No. 5.6e-09;
Conservative 0; Mismatches 1;
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/dev_stage="Adult"
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High quality sequence start: 103
High quality sequence stop: 460.
Location/Qualifiers
/clone_lib="GN0166"
                        /dev_stage="Adult"
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BG015966.1 GI:12468699
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                                                    BG014975
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                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 482)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtm12.pl?tl=CM2&t2=CM2-GN0166-
101100-496-905&t3=2000-11-10&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 20
High quality sequence stop: 130.
Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shotgun sequencing of the human transcriptome with ORF expressed
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Sequence tags
20202663
                                                      Length 460;
                                                                                               Indels
                                                        DB 10;
                                                        Score 58.4; DB 10
Pred. No. 5.6e-09;
0; Mismatches 1

    .482
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BF998626.1 GI:12434248
                                                        97.3%;
98.3%;
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Best Local Similarity
Matches 59; Conserv
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/note="Organ: placenta_normal; vector: puc18; Site_1: Smal ; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 500)
Dias Neto,E., Garcia,R., Verjovski-Almeida,S., Briones,M.R., Magai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
Shotgun Sequencing of the human transcriptome with ORF expressed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC4&t2=RC4-GN0323-211200-021-f01&t3=2000-12-21&t4=1)
BG014975 . 500 bp mRNA linear EST 24-JAN-2001
RC4-GN0323-211200-021-f01 GN0323 Homo sapiens CDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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20202663
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Pred. No. 5.7e-09;
0; Mismatches 1;
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/db_xref="taxon:9606"
/clone_lib="GN0323"
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High quality sequence stop: 500.
Location/Qualifiers
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BE874824
BE874824.1 GI:10323600
EST.
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BG014975.1 GI:12466715
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Best Local Similarity 98.3%;
Matches 59; Conservative
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Gaps

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Indels

Length 557;

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/organism="Homo sapiens"
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/note="Organ: adrenal gland; Vector: pCMV-SpORT6; Site_1:
primed. Average insert size 1.229 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NHH MGC Library."

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Pred. No. 5.9e-09;
0; Mismatches 1;
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98.3%;
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Fax: +55-11-2707001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST 22-JAN-2001
                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 553)
MNH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) (Uppublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 557)
NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BF970308 557 bp mRNA linear EST 22-JAN-
602273694F1 NIH_MGC_84 Homo sapiens cDNA clone IMAGE:4361638 5'
                                                                                                                                                                                Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
tolumn: 18
High quality sequence stop: 540.
Location/Qualifiers
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Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLANLOGO4 row: I column: 23
High quality sequence stop: 556.
Location/Qualifiers
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/organism="Homo sapiens"
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FMAX: 1-31-11-14/VUVUL

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RCO&t2=RCO-CTO380-
070100-031-904&t3-2000-01-07&t4-1)
Seq primer: puc 18 forward
High quality sequence start: 28
High quality sequence stop: 570.

Location/Qualifiers
1. .570

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/note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2:
And Ring Products derived
From ORESTES PCR (U.S. Letters Patent appliantion No. 196
716 - T. .74-17 Tout Freithte for Cancer Research) profiles
AW579074 570 bp mRNA linear EST 16-MAR-2000 RC0-CT0380-070100-031-904 CT0380 Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                           Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutherla, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 570)
HCGP http://www.ludwig.org.br/ORESTES.
The PAPESP/LICR Human Cancer Genome Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Best Local Similarity
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source

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCMI767 row: o column: 17
High quality sequence stop: 575.
Location/qualiflers
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Pred. No. 6e-09;
0; Mismatches 1; Indels 0
  1; Indels
Mismatches
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Tissue Procurement: ATCC
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Best Local Similarity 98.3%;
Matches 59; Conservative (
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/tissue_trpe="repithelioid carcinoma cell line"
/lab_host="Publib (phage-resistant)"
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Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp following 5' adaptor: GGACGAG(G). Library constructed by Ling for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. |"
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA,Sequencing by: Incyte Genomics, Inc.
clone distribution: MGC clone distribution information can be
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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http://image.llnl.gov
plate: LLCM1830 row: f column: 06
High quality sequence start: 6
High quality sequence stop: 582.
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Pred. No. 6e-09;
0; Mismatches 1;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5017733"
/clone_lib="NIH_MGC_42"
                                                                                                       Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC
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Best Local Similarity 98.3*
Matches 59; Conservative
                                                                                    Unpublished (1999)
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Sequence:

Run on:

Searched:

Database

Result

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AI888176 wm40b06.x
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length.cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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                            GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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/tissue_type="B cells from Burkitt lymphoma"
/note="Vector: pcwySpRT 6; Site_1: Not!; lst strand cDNA
was primed with a Not!-Oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
colned into the Not I and Eco RV sites of the pcwySpORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Diive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email: fliang@lifetech.com URL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
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996 bp mRNA linear EST 16-FEB-2001
Homo sapiens cDNA clone CSODL007F12 3
                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 996)

Lij, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

Contact: Genoscope
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Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="CSODLOO7F12"
/clone=lb="LTI_NFL010_BC2"
/sex="male"
    AL582634 LTI_NFL010_BC2
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AL582634.1 GI:12950809
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AL542659.1 GI:12874922
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GTGTGCTGCGAGGATCGCCAGCACTGCTGCCGGCTGGCTACACCTCCAACGTGAAGGCT
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqrefégenoscope.cns.fr, Web : www
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
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Mammalla; Eutheria; Primates;
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and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Life rechnologies. Context: Fernologies, a division of Invitrogen 9800 Medical Center Drive Rockville Maryland 20850, USA Fax : (1) 301 610 8371 Email : filang@lifetech.com URL : 3 others % 131 c 287 g 176 t 3 others %
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..8e-188;
nes 15;
                                                                                                            Score 860.8; I
Pred. No. 1.8e-
3; Mismatches
                                                                                                            ch 80.3%; 11 Similarity 97.7%; 901; Cónservative 3
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618

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887 bp mRNA linear EST 16-FEB-2001
Homo sapiens cDNA clone CSODIO81XC03 3
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Catarrhini; Hominidae; Homo.
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Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
ggacacttctgccatgataaccagacctgctgccgagacaaccgacagggctgggcctgc
                                                                                                                                                                      GRAMACTICTGCCATRATAACCAGACCTGCTGCCGAGACAACCGACGGGCTGGGCTGC
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Mammalia; Eutheria; Primates; Catarrhini; Hoi
1 (bases 1 to 887)
Lii,W.B., Gruber,C., Jessee,J. and Polayes,D.
Unil-length cDNA libraries and normalization
Unpublished (2001)
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AL576991
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AUTHORS
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was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email: filiang@lifetech.com URL:
http://fullelepth.invitrogen.com"
- 260.
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1 (bases 1 to 900)

14, W.B., Gruber.C., Jessee,J. and Polayes,D.

14, M.B., Gruber.C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished (2001)

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr.
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enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: filiang@lifetech.com URL: http://fulliang@lifetech.com URL: http://fulliang@lifetech.com a 277 c 288 g 151 t 11 others
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                                                                                                                               2,
                                                                                                            Length 887;
                                                                                                             71.4%; Score 765; DB 9; I 94.3%; Pred. No. 2.3e-166; iive 5; Mismatches 41;
                                                                                                                     Local Similarity 94.3
Les 838; Conservative
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E 1 (bases 1 to 810)

NI HOGS http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

NI Onpublished (1999)

Contact: Moobert Strausberg, Ph.D. Contact: Louis M. Staudt, M.D., Ph.D. Consortium (LIML)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

http://image.llnl.gov

Plate: LLCM1619 row: h column: 04

High quality sequence stops 810.

Location/Qualifiers
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/clone=lib="NIH_MGC.48"
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/tissue_ttpe="primary B-cells from tonsils (cell line)"
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/tissue_ttpe="primary B-cells vector: portary site_1: xho!;
/note="forgan: B-cells; vector: portary: site_1: xho!;
/note="forgan: B-cells; vector: portary site_1: xho!;
/note="forgan: B-cells; vector: portary site_1: xho!;
/note in a forgan: B-cells; vector: portary: site_selected >500pp
/for average insert size 1.8kb. Library constructed by Ling
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(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NHH_MGC Library."
// A a 257 c 265 g 147 trary."
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0; Mismatches 16; Indels
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/lab_host="DH108"
/note="Crgan: brain; Vector: pCMVSPORT 6; lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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Genoscope - Centre National de Sequencage
BP 191 91006 FVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.
Location/Quallifiers
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AL562633 LTI_NFL003_NBC3
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vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: filangelifetech.com URL: http://fulllength.invitrogen.com a 292 c 296 g 157 t 10 others
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Pred. No. 1.6e-164;
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/clone="csobn03xc04"
/clone="csobn03xc04"
/clone="tsobn103xc04"
/cloned into the Not! and Eco Rv sites of the pcWvSpORT 6
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Eil,W.B., Gruber,C., Jessee,J. and normalization
Unpublished (2001)
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BP 191 91006 KYRX cedex - France
Emall: segrefégenoscope.cns.fr. Web : www.genoscope.cns.fr.
Location/Qualifiers
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Pred. No. 3.2e-162;
6; Mismatches 22; Indels
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/clone_lib="ITI_NED06_PL2"
/tissue_type="placenta"
/tissue_type="placenta"
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/tissue_type="placenta"
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/oote="vector: pCwNsPORT 6; Site_l: NotI; lst strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AL575030 ALT_NFL006_PL2 Homo sapiens cDNA clone CSODIO64YN13 3
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                  680 gctgcgcacgcaggggtaccaagtgtttgcgcagggaggccccgcgctgggacgccctt
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                                                                                                                                                                                                                                                               620 gtccctacgcccagggcgtctgttgtgctgatcggcgccactgctgtcctgctggcttcc
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Contact: Genoscope
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BP 191 91006 EVR cedex - France
Email: seqrefégenoscope.cns.fr, Web : www.
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="CSODI064YN13"
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AL575030
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BASE COUNT ORIGIN

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// Corganism="Homo sapiens"
// Ab_xref="taxon:9606"
// Clone="InAGE:4861255"
// Clone="InAGE:4861255"
// Clone="InH_MGC_49"
// Issue_type="melanotic melanoma, high MDR (cell line)"
// Ab_host="DH10B (phage-resistant)"
// Ab_host="Dh1
                                            Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 780)

8 NIH-MoC http://mgc.nci.nih.gov/.

8 NIH-MoC http://mgc.nci.nih.gov/.

1 Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: ATC/CDTD/DTP

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

http://image.llnl.gov

Plate: LLCM/19 row: n column: 08

High quality sequence stop: 777.
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Pred. No. 2.2e-154;
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Best Local Similarity 97.7%;
Matches 755; Conservative 0
                         Homo sapiens
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Email: cgapbs-rémail.nih.gov
    Tissue Procurement: ATCC/DCTP/DTP
    CDNA Library Preparation: Ling Hong/Rubin Laboratory
    CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
    DNA Sequencing by: Incyte Genomics, Inc.
    Clone distribution: MGC Clone distribution information can be
    found through the I.M.A.G.E. Consortium/LINL at: image.llnl.gov
    plate: LLCMA27 row: c column: 23
    High quality sequence stop: 740.
    Aloration/Qualifiers
    I. 745
    Corganism="Homo sapiens"
    Ab_xref="taxon:9606"
    //db_xref="taxon:9606"
    //db_xref="taxon:9606"
    //db_xref="fallone" librage-resistant;"
    //db_nost="fallone" librage-resistant;"

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Pred. No. 3.2e-150;
0; Mismatches 16;
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Best Local Similarity 97.6%;
Matches 726; Conservative
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 807)
NHT-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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caggitgccctggatggagaaggccccagctcacctccagcctgccagacccacaagccttg
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BE742164.1 GI:10156156
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Tissue Procurement: DCTD/DTP
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717

804

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GCAGCCAGGGTACCAAGTGTTTGCGCAGGGAGGCCCCGCGCTGGGACGCCCCTTTGAGG 660
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ORIGIN
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TITLE
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                                                                                                                                                                                                                                                                                                                      /tissue_type"adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: ovary; Vector: pOTB7; Site_1: XhoI; Site_2:
/note="Organ: ovary; Vector: poTB7; Site_1: XhoI; Site_2: ovary; Note o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3;
cDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incytt Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM520 row: d column: 15
High quality sequence start: 3
High quality sequence stop: 790.
Location/Qualifiers
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Pred. No. 7.6e-150;
0; Mismatches 21;
                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
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/clone_lib="NIH_MGC_9"
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milarity 96.7%; F
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Anote-"Organ: pooled lung and spleen; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA source anonymous pool of 24 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dr primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C Gruber (Invitrogen). Research Genetics tracking code 026. Note: this is a NIH,MGC Library."
BIS24853 894 bp mRNA linear EST 29-AUG-2001
60305187611 NIB_MGC_122 Homo sapiens chNA clone IMAGE:5201346 3',
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NIH-MGC http://mgc.ncl.nih.gov/.

National institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cona Library Preparation: Life Technologies, Inc.

cona Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://mage.llnl.gov

Plate: LLAM11504 row: h column: 19

High quality sequence start: 23

High quality sequence start: 23

High quality sequence stop: 830.

Location/Qualifiers

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                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
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/clone="IMAGE:5201346"
/clone_lib="NIH_MGC_122"
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                                                                                    BI524853
BI524853.1 GI:15349645
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                                                            mRNA sequence.
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602764696F1 NIH_MGC_42 Homo saplens cDNA clone IMAGE:4906991 5',
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NIH-MGC http://mgc.nci.nih.gov/.
Nith-MGC institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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                774 CGTGGCTGGACCTGGAGAATAATGCCTGCCGGCGGGCTTCCTGATCCCACCCCCAGAGAC
                                 gtgtggggaaggacacttctgccatgataaccagacctgctgccgagacaaccgacaggg
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Tissue Procurement: ATCC
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cDNA Library Preparation: Ling Hong/Rubin Laboratory

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Pred. No. 3.4e-145;
0; Mismatches 23;
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Best Local Similarity 96.5%;
Matches 720; Conservative
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5087479"
/clone=lib="NIH_MGC_100"
/tlssue_type="hepatocellular carcinoma, cell line"
/tab_host="hepatocellular carcinoma, cell line"
/tab_host="hepatocellular carcinoma, cell line"
/tote="Organ: liver; Vector: pOTB7; Site_1: XhOI; Site_2:
ECORI.cDNA made by oligo-dr priming. Directionally cloned
into ECORI/XhOI sites using the following 5' adaptor:
GGCACGAG(G). Size=selected >500bp for average insert size
1.8kb_ilbrary constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
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602953132T1 NIH_MGC_100 Homo saplens CDNA clone IMAGE:5087479 3',
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                              Email: cgapbs-remail.nih.gov
Tissue Procurement: CGAP (Stanford)
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genemics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/Link at:
http://image.llnl.gov
Plate: LLCM1844 row: p column: 08
High quality sequence start: 23
High quality sequence stop: 846.
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
                                                                                                            BI253057.1 GI:14804112
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Search completed: September 5, 2002, 15:34:19 Job time: 8757 sec Appli Appli Appli Appli Appli

Sequence Seq

Sequence 19,

OM nucleic

Run on:

Sequence:

Searched:

Database

Result

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Sequence 16, Application US/08991862
Patent No. 6309826
GENERAL INFORMATION:
TITLE OF INVERTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 29996.488/P001-A
CURRENT APPLICATION NUMBER: US/08/991,862
CURRENT FILING DATE: 1998-08-17
EARLIER PLING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                s sequence of human granulin/epithelin (human GP88). Human Granulin Genebank
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US-08-822-028-72
US-08-109-106-4
US-08-109-106-4
US-08-109-106-1
US-08-461-968A-1
US-08-461-968A-1
US-08-462-571-1
PCT-US96-10043-8
US-08-44-18
US-08-322-46A-18
US-08-322-346A-18
US-08-322-346A-18
US-08-323-246A-18
US-08-35-576-25
US-08-362-670B-25
US-08-362-670B-25
US-08-362-670B-25
US-08-362-670B-25
US-08-363-376-25
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US-09-105-537-32
US-09-105-537-9
US-09-320-878-19
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NAME/KET: CDS
LOCATION: (13)..(1791)
OTHER INFORMATION: Nucleotide se;
OTHER INFORMATION: precursor (hu
OTHER INFORMATION: #75161.
US-08-991-862-16
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LENGTH: 2095
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
                   GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-429-998-3
US-08-431-333-3
US-08-91-862-1
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US-08-429-998-1
US-08-431-333-1
US-08-431-333-1
PCT-US91-02321-1
US-07-668-648-5
US-08-429-998-5
US-08-429-998-5
US-08-431-333-5
PCT-US91-02321-7
US-08-431-333-7
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US-08-431-333-7
US-08-431-333-9
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Listing first 45 summaries
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Patent No. 5416192
GENERAL INFORMATION:
APPLICANT: Showa, Mohammed
APPLICANT: Plowman, Gregory D.
TITLE OF INVENTION: MODULATING PROTEINS
ITLE OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the Americas
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STREET: 1155 Avenue of t
CITY: New York
STATE: New York
COUNTRY: USA
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US-07-668-648-3
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

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Pred. No. 2.9e-175;
0; Mismatches 13;
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION NUMBER: US/07/668,648
FILLNG DATE: 19910819
CLASSIFICATION: 514
                                                                                             ATTORNEY AGENT INFORMATION:
NAME: MISTOCK, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DECKET NUMBER: 5624-161-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 869-9741
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1779 base pairs
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 69.7%;
Best Local Similarity 98.3%;
Matches 755; Conservative
                                                                                                                                                                                                                                                          single
                                                                                                                                                                                                                                                                                   MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapi
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TISSUE TYPE: Kidney
                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: CDS
LOCATION: 1..1779
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CURRENT APPLICATION DATA:
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. 1 gggccccaccaggtgcctggatggagaaggccccagctcacctcagcctgccagaccca 60
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Patent No. 5885961
GENERAL INFORMATION:
APPLICANT: Shoyab, Mohammed
APPLICANT: PLOWMAN, Gregory D.
TITLE OF INVENTION: RETHELINS: NOVEL CYSTEINE-RICH GROWTH
TITLE OF INVENTION: MODULATING PROTEINS
NUMBER OF SEQUENCES: 12
                                                                                                                                             1732 CCGCGCTGGGACGCCCCTTGAGGGACCCAGCCTTGAGACAGCTGCTG 1779
                                                                                                                             721 ccgcgctgggacgccctttgagggacccagccttgagacagctgctg 768
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/429,998
FILING DATE: 27-APR-1995
CLASSIFICATION: 514
PRIOR APPLICATION NUMBER: US 07/668,648
FILING DATE: 13-AAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Mistock, S. Leslie
REGISTRATION NUMBER: 5624-161-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)790-9090
TELEPHONE: (212)790-9090
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)790-9090
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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Pred. No. 2.9e-175;
0; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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98.3%;
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Best Local Similarity 98.3
Matches 755; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE TYPE: Kidney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: CDNA ORIGINAL SOURCE:
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US-08-429-998-3
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US-08-429-998-3
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421 cyccaycactyctycccyyctygctacacctycaacytyaayyctcyatcctycyayaay
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; Patent No. 5965723
; GENERAL INFORMATION:
; APPLICANT: Blowan Gregory D.
TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
TITLE OF INVENTION: MODULATING PROTEINS
; UNMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1155 Avenue of the Americas
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1072 CAAGCCTTGAAGAGAGAGATCTCCCTGTGATAATGTCAGCAGCTGTCCCTCCTCCTGGAAGC 1131
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                              1612 CGACAGGGCTGGGCCTGCTGTCCCTACCGCCAGGGCGTCTGTTGTGCTGATCGGCGCCAC 1671
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cgacagggctggcctgctgccctacgcccagggcgtctgttgtgctgatcggcgccac
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PCT-U591-02321-3
Squence 3, Application PC/TUS9102321
SGQUENCE 1 PLOWMAN 10N:
APPLICANT: Shoyab, Mohammed
APPLICANT: Plowman, Gregory D.
TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
TITLE OF INVENTION: MODILATING PROTEINS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 19910403
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: POOT, BILAN W.
REGISTRATION NUMBER: 32,928
REFERENCE/POOCKET UNBER: 32,928
TELECOMMULCATION INFORMATION:
TELECOMMULCATION INFORMATION:
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Pred. No. 2.9e-175;
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                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Bristol-Myers Squibb Company
STREET: 3005 First Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 98121
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release
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98.3%;
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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Matches 755; Conservative
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1..1779
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                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Seattle
STATE: Washington
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; LOCATION:
PCT-US91-02321-3
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Pred. No. 2.9e-175;
0; Mismatches 13;
                                            PRICE APPLICATION DATA:

APPLICATION NUMBER: US 07/668,648
FILING DATE: 13-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 16,872
REFERENCE/DOCKET NUMBER: 5624-161-99
RELEPHONE: (212)790-9090
TELEPHONE: (212)790-9090
TELEPHONE: (212)790-9090
TELEPHONE: (212)786-9741
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1779 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPPOLOGY: 11near
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98.3%;
                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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Best Local Similarity 98.3
Matches 755; Conservative
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                                  CLASSIFICATION: 536
APPLICATION NUMBER:
FILING DATE: 27-APF
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US-08-431-333-3
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NAME/RET: COSTION: (23)...(1789)

COCHEN INFORMATION: The sequence is identical to that of the published OTHEN INFORMATION: mouse granulin except for one nucleotide (T OTHEN INFORMATION: instead of G) at position 1071 of GP88 CDNA US-08-991-862-1
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Patent No. 6309826
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TILE REFERENCE: 20996.488/P001-A
TILE REFERENCE: 20996.488/P001-A
CURRENT APPLICATION NUMBER: 02/08/991,862
CURRENT FILING DATE: 1999-08-17
EARLIER PILING DATE: 1999-08-17
SALIER PILING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1.2
                                                cgacagggctgggcctgctgtccctacgcccaggcgtctgttgtgctgatcggcgcac
1132 TGCTGCCAACTCACGTCTGGGGAGTGGGGCTGCTGTCCAATCCCAGAGGCTGTCTGCTGC
                                                                                                                                                     caccccagagacatcggctgtgaccagcaccagctgcccggtggggggaacctgctgc
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US-08-991-862-1
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                                                                                                                              ggtatcctccaagtagggtggatgaagaaggtcatagcccccctccgcctgccagaccca
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                                                  15;
              Length
                                                    Indels
Score 533.8; DB 4;
Pred. No. 1.1e-122;
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                                                      0; Mismatches
                49.8%;
71.8%;
                Query Match 49.8
Best Local Similarity 71.8
Matches 758; Conservative
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RESULT 8
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                                                                                                                             APPLICANT: Shoyab, Mohammed
APPLICANT: Shoyab, Mohammed
APPLICANT: Plowar, Gregory D.
APPLICANT: PLOWER, EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
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                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/668,648
FILING DATE: 19910819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 469.2; DB 1;
Pred. No. 8.6e-107;
0; Mismatches 173;
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: L.J.L.
CLASSIFCATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MISTOCK, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624
TELEPONE: (212)790-9090
TELEFAX: (212) 869-9741
: INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHRRACTERISTICS:
LENGTH: 1767 base pairs
                                                                                         Sequence 1, Application US/07668648
Patent No. 5416192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 43.8%;
Best Local Similarity 76.7%;
Matches 589; Conservative
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                                                                                                                                                                      TITLE OF INVENTION: EP TITLE OF INVENTION: MOI NUMBER OF SEQUENCES: 1. CORRESPONDENCE ADDRESS:
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                                                                                                                        GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                   USA
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                                                                                                                                                                                                                                                                                                                10036
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US-07-668-648-1
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                                                                            US-07-668-648-1
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Patent No. 5885961
GENERAL INFORMATION:
APPLICANT: Shoyab, Mohammed
APPLICANT: Plowman, Gregory D.
TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
TITLE OF INVENTION: MODULATING PROTEINS
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REGISTRATION NUBBER: 18,872
REFERENCE/DOCKET NUMBER: 5624-161-999
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ve.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/429,998
FILING DATE: 27-ARR-1995
CLASSIFICATION: 514
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APPLICATION NUMBER: US 07/668,648
FILING DATE: 13-MAR-1991
ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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ADDRESSEE: Pennie & 1
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GENERAL INFORMATION:
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                                                                                                                                             Indels
                                                                                                                       Score 469.2; DB 2;
Pred. No. 8.6e-107;
0; Mismatches 173;
                                                                                                                        Query Match
Best Local Similarity 76.7%;
Matches 589; Conservative
 1767 base pairs
         TYPE: nucleic acid
STRANDENNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
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                                                                      HAME/KEY:
COCATION:
US-08-429-998-1
  LENGTH:
                                                             FEATURE
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; Sequence 1, Application US/08431333 ; Patent No. 5965723

US-08-431-333-1

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                                          NOVEL CYSTEINE-RICH GROWTH
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nilarity 76.7%; Pred. No. 8.6e-107;
Conservative 0; Mismatches 173;
                                                                                                                                                                                                                                                                                                                  #1.25
                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/POCKET NUMBER: 564-161-999
TELECOMUNICATION INFORMATION:
TELEPHONE: (212)790-909
TELEPAX: (212) 869-9741
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1767 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
APPLICANT: Shoyab, Mohammed
APPLICANT: Shoyab, Mohammed
APPLICANT: Plowman, Gregory D.
TITLE OF INVENTION: EPITHELINS: NOVEL CN
TITLE OF INVENTION: MODULATING PROTEINS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
                                                                                                                    E: Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, N
CURRENT APPLICATION DATA:
APPLICATION MUMBER: US/08/431,333
FILING DATE: 27-APR-1995
CLASSIFICATION: 536
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APPLICATION NUMBER: US 07/668,648
FILING DATE: 13-MAR-1991
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                             CITY: New York STATE: New York
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LOCATION:
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                                                                                                                                                                                                                                                                                        1660 TGTTGTCCCATTGGCTTCCACTGTTCAGCCAAGGGAACCAAGTGTTTGCGGAAGAAGC 1719
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                                                                                                                                                                 gacgiggagigtgigggaaggacactictgccaigataaccagacctgctgccgagacaac 600
                                                    cgccagcactgctgcccggctggctacacctgcaacgtgaaggctcgatcctgcgagaag
                                                                    gaagtggtctctgcccagcctgccaccttcctggccgtagccctcacgtgggtgtgaag
  tgctgtcctgctggcttccgctgcgcacgcaggggtaccaagtgtttgcgcagggaggcc
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application PC/TUS9102321
GENERAL INFORMATION:
APPLICANT: Shoyab, Mohammed
APPLICANT: Plowman, Gregory D.
TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
TITLE OF INVENTION: MODULATING PROFIENS
                                                                                                                                                                                                                                                                                                                                                721 ccgcgctgggacgccctttgagggacccagccttgagacagctgctg 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/02321
FILING DATE: 19110403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Bristol-Myers Squibb Company
STREET: 3005 First Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 19910403
CLASSIFICATION: 514
ATTORNEY AGENT INFORMATION:
NAME: POOR, Brian W.
REGISTRATION NUMBER: 32,928
REFERENCE/DOCKET NUMBER: 0N0071A-PC
TELECOMMUNICATION INFORMATION:
TELEFAX: (206)728-4800
TELEFAX: (206)448-4775
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 1767 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: EP
TITLE OF INVENTION: MO
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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MOLECULE TYPE: CD
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STATE: Washing
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TISSUE TYP
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PCT-US91-02321-1
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 Length 1767;
Indels 6;
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US-07-668-648-5

US-07-668-648-5

Sequence 5, Application US/07668648

Patent No. 5416192

GENERAL INFORMATION:

APPLICANT: Shoyab, Mohammed

APPLICANT: Plowman, Gregory D.

TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH

TITLE OF INVENTION: MODULATING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1720 CCTCGCTGGGACATACTTTGAGGGATCCAGCCCCAAGACCGCTACTG 1767
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Score 469.2; DB 5;
Pred. No. 8.6e-107;
0; Mismatches 173;
 43.88;
                                       Conservative
                    Similarity
 Query Match :
Best Local Simi
Matches 589;
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1426 CGGCAGCACTGTTGCCCGGCCGGGTACACCTGCAATGTGAAGGCGAGGACCTGTGAGAAG 1485
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1155 Avenue of the Americas
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                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Shoyab, Mohammed
APPLICANT: Plowman, Gregory D
TITLE OF INVENTION: EPITHELIN
TITLE OF INVENTION: MODULATIN
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie 6 Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Mus musculus
TISSUE TYPE: Kidney
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STRANDEDNESS: single
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LOCATION: 1.1767
JS-08-429-998-5
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CITY: New York
STATE: New York
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41.8%; Score 448.4; DB 1; Length 1767;
Best Local Similarity 75.0%; Pred. No. 1.1e-101;
Matches 576; Conservative 0; Mismatches 186; Indels 6;
                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                             ATTORNEY AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624-161-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)790-9090
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1767 base pairs
   CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                APPLICATION NUMBER: US/07/668,648
FILING DATE: 19910819
                                                                                                                         MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Polocal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: NUCLEIC ACID.
                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE TYPE: Kidney
                                                                                                                                                                                                                                 FILING DATE: 199108
CLASSIFICATION: 514
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                                                                    New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY: CDS
; LOCATION: 1...1
US-07-668-648-5
                                                                                   USA
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Gregory D.
EPITHELINS: NOVEL CYSTEINE-RICH GROWTH MODULATING PROTEINS: 12
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MEDIUM TYPE: FIPPPY disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: TEM PC COMPATIBLE
COMPUTER: PAtentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/429,998
FILING DATE: 27-APR-1995
CLASSIFICATION NUMBER: US/0666,648
FILING DATE: 13-APR-1991
ATTORNET/AGENT INFORMATION:
ANAME: MASIOCAE NUMBER: 5624-161-999
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 5:
SEQUENCE (ABRACTERISTICS:
LEMSTH: 1767 base pairs
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COMPUTER READABLE FORM:
New York
                    ZIP: 10036
         COUNTRY:
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                    Length 1767;
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Patent No. 5965723

GENERAL INFORMATION:
APPLICANT: APPLICANT: Plowman, Gregory D.
TITLE OF INVENTION: EPTHELINS: NOVEL CYSTEINE-RICH
TITLE OF INVENTION: MODULATING PROTEINS
                    Score 448.4; DB 2;
Pred. No. 1:1e-101;
0; Mismatches 186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3: Pennie & Edmonds
1155 Avenue of the Americas
                   Query Match 41.8%;
Best Local Similarity 75.0%;
Matches 576; Conservative
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ADDRESSEE: Pennie &
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121 tgctgccaactcacgtctggggagtggggctgctgtccaatcccagaggctgtctgctgc 180
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                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CAPLICATION NUMBER: US/08/431,333
FILING DATE: 27-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
41.8%; Score 448.4; DB 2;
Best Local Similarity 75.0%; Pred. No. 1.1e-101;
Matches 576; Conservative 0; Mismatches 186;
                                                                                                                                                                         APPLICATION NUMBER: US 07/668,648
FILING DATE: 13-MAR-1991
ATTORNEY/AGENT INFORMATION:
MEDIUM TYPE: Floppy disk
Compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                   NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 565
TELECOMMUNICATIÓN INFORMATION:
TELEPHONE: (212)790-9090
                                                                                                                                                                                                                                                                                                                               TELEFAX: (212) 869-9741
INFORMATION FOR SEG ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 1767 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Mus musculus
                                                                                                                FILING DATE: 27-APR-1
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE TYPE: Kidney
                                                                                                                                                                                                                                                                                                                                                                                                                   nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; NAME/KEY:
; LOCATION:
US-08-431-333-5
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US-07-668-648-7
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                               1486 GATGTCGATTTTATCCAGCCTCCGTGCTCCTGACCCTCGGCCCTAAGGTTGG----G
                                                                     541 gacgtggagtgtggggaaggacacttctgccatgataaccagacctgctgccgagacaac
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gaagtggtctctgcccagcctgccaccttcctggcccgtagccctcacgtgggtgtgaag
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Sequence 5, Application PC/TUS9102321

GENERAL INFORMATION:
APPLICANT: Showman, Gregory D.
TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
TITLE OF INVENTION: MODULATING PROTEINS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                   1720 CCTCGCTGGGACATGTTTTTGAGGGATCCGGTCCCAAGACCGCTACTG 1767
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MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: PCT/US91/02321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Bristol-Myers Squibb Company
STREET: 3005 First Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ON0071A-PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: POOT, Brian W.
REGISTRATION NUMBER: 32,928
REFERENCE/POCKET UNMBER: ON00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)728-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (206)448-4775
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1767 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Mus musculus
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STRANDEDNESS: single
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CITY: Seattle
STATE: Washington
COUNTRY: USA
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CLASSIFICATION:
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PCT-US91-02321-5
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481
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Gaps

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Indels

Best_Local Similarity 75.0 Matches 576; Conservative

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                                                                                                            1366 CCAAGCCTCAAGGGAAGTTGGGCCTGCTGCCAGCTGCCCCATGCTGTGTGAGGAC
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                                                      caagcettgaagagagatgteeetgtgataatgteageagetgteeeteeteegataee
gggccccaccaggtgccctggatggagaaggccccagctcacctcagcctgccagaccca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH TITLE OF INVENTION: MODULATING PROTEINS NUMBER OF SEQUENCES: 12 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1720 CCTCGCTGGGACATGTTTTGAGGGATCCGGTCCGACCGCTACTG 1767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ccgcgctgggacgccctttgagggacccagccttgagacagctgctg 768
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STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7, Application US/07668648
Patent No. 5416192
GENERAL INFORMATION:
APPLICANT: Shoyab, Mohammed
APPLICANT: Plowman, Gregory D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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OM nucleic - nucleic search, using sw model

September

Run on:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0

Scoring table:

Searched:

Perfect score:

Sequence:

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PAT 17-DEC-2001
                                                                                                                                                                                    R.norvegicu
Rattus norv
                                                                                                                                                                                                                                                                                                                                                                           AC025326 Homo sapi
AL566258 Mus muscu
AX198393 Sequence
AX208943 Sequence
AR079657 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AF429315 Homo sapl
AR079658 Sequence
111833 Sequence 9
AF429315 Homo sapi
281595 Caenorhabdi
            M75161 H.sapiens g
BG01657 Homo sapi
X62320 H.sapiens m
AF055008 Homo sapi
AK006607 Homo sapi
AK02348 Homo sapi
                                                                                                              111830 Sequence 3
AC003043 Homo sapi
L01117 Human granu
AC019151 Homo sapi
AC019151 Homo sapi
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AC091303 Homo sapi
M86735 Guinea pig
D16195 Mouse gene
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AR079654 Sequence
111829 Sequence
AR079656 Sequence
111831 Sequence 5
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AP000058 Aeropyrum
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Continuation (9 of
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G54019 922 Human
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AC090454 Homo sapi
AR175456 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88kDa tumorigenic growth factor and antagonists Patent: US 6309826-A 16 30-OCT-2001; Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AR175456 2095 bp
Sequence 16 from patent US 6309826.
AR175456.
AR175456.1 GI:17916755
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LMFLCHR18_08
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HUMGRANULI
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AR079655
I11830
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AR175447
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1 (bases 1 to 2095)
Serrero,G.
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58.7 139488
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Best Local Similarity
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Unknown.
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ACCESSION
VERSION
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SOURCE
ORGANISM
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ORIGIN
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TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
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                                                                                                  ; Search time 3362.64 Seconds (without alignments) 6671.320 Million cell updates/sec
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                                                                                                                                                                                                                                                                                           3595312
                GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                             1797656 seqs, 10463268293 residues
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                                                                                                    5, 2002, 16:30:39
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Listing first 45 summaries

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GenEmbl: *

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Database

gb_ov:* gb_pat: gb_ph:*

ap_om:

gb_ro:* gb_sts:

gb_pl:* gb_pr:*

gb_sy:* gb_un:*

em_fun:

em_hum

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em_ba:

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em_om:*

em_pat: em_pl:

em_ph:

em_ov:

em mu:

Post-processing: Minimum Match 0% Maximum Match 100%

Minimum DB seq length: 0 Maximum DB seq length: 200000000

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em_htg_inv:*
em_htg_other:*

em_sts:

em_un:

em_ro:

em_htgo_inv:*

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Query Score Match Length DB

Result . ₽

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/668,648
FILING DATE: 19910819
CLASSINFORMY INFORMATION:
NAME: Misrock, S. Leslie
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624-161-999
TELECOMMUNICATION INFORMATION:
TELEPRAX: (212) 869-9741
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 539 base pairs
TYPORDINESS: SIGGLE
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
ORGANISM: Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Bos tauru:
TISSUE TYPE: Kidney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; NAME/KEY:
; LOCATION:
US-07-668-648-7
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 Score 153.2; DB 1;
Pred. No. 4.3e-29;
0; Mismatches 33;
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                                                                                                                                                                                                                                               508 rcgaccaccaccacrecretccca 533
Ouery Match
Best Local Similarity 84.0%;
Matches 173; Conservative
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Length 539;

Search completed: September 5, 2002, 18:22:29 Job time: 13352 sec

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1. .2095
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                                                                                                                                                                                                      Location/Qualifiers
1. 2095
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13. .1794
                                                 granulin mRNA,
                                                                     M75161.1 GI:183612
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                               1024 GGGCCCACCAGGTGCCTGGATGGAGGAGGCCCCAGCTCACCTCAGCCTCAGCCTCAGCCCAGACCCA 1083
                                                                                                    1624 CGACAGGGCTGGCCTGCTGTCCCTACGCCCAGGGCGTCTGTTGTGCTGATCGGCGCCCAC 1683
                                                                               CAAGCCTTGAAGAGAGATGTCCCCTGTGATAATGTCAGCAGCTGTCCCTCCTCCGATACC 1143
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                      gggccccaccaggtgccctggatggagaaggccccagctcacctcagcctgccagaccca
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ARSPHVGKNDVEGEGGHFGHDNVCCEDNRQGWACCPYAQGVCCADRRHCCPAGFRCA ö PRI 31-DEC-1994 marrow Euteleostomi; Homo. human caagccttgaagagagatgtcccctgtgataatgtcagcagctgtccctcctccgatacc 120 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleo Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo. I (bases 1 to 2095)
Bhandari, V., Palfree, R.G. and Bateman, A.
Isolation and sequence of the granulin precursor cDNA from bone marrow reveals tandem cysteine-rich granulin domains Proc. Natl. Acad. Sci. U.S.A. 89 (5), 1715-1719 (1992) 1084 CAAGCCTTGAAGAGAGATGTCCCCTGTGATAATGTCAGCAGCTGTCCCTCCGATACC Homo sapiens (tissue library: Clontech HL1058b) adult bone ö Length 2095; Indels linear

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIANL at: http://image.llnl.gov Series: IRAK Plate: 12 Row: a Column: 17 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 10435243. Location/Qualifiers
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                            Submitted (10-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact:'villalon@bcm.tmc.edu.
Villalon; D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., G
A.M., Holloway, M., Telford, B, Hodgson, A., Bouck, J., Yu,
Muzny, D.M., Glbbs, R.A.
                                                                                                                                                                                               NIH-MCC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Contact: MGC help desk
Email: capabs-remail.nih.gov
Tissue Procurement: ATCC
CONA Library Preparation: Life technologies, Inc.
CONA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
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Pred. No. 3.3e-216;
0; Mismatches 14;
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Strausberg, R.
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clone MGC:9342 IMAGE:3457813, mRNA,
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CEQGPHQVPAMEKAPAHLSLPDPQALKRDVPCDNVSSCPSSTCCQLTSGEWGCCPIP
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ARSPHYGVKDVBCGEGHFCHDNQTCCRDDNRQGWACCPFTRQGVCCADRRHCCPAGFRCA
Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                            Submitted (15-JAN-1991) G.D. Plowman, Oncogen, 3005 1st Avenue, Seattle, WA 98121, U S A See also X62320-2.
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                                                                                               with opposing
                  Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2152)
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                                                  Plowman, G.D., Green, J.M., Neubauer, M.G., Buckley, S.D., McDonald, V.L., Todaro, G.J. and Shoyab, M. The epithelin precursor encodes two proteins with opposactivities on epithelial cell growth J. Biol. Chem. 267 (18), 13073-13078 (1992)
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1. 2152
7. Corganism="Homo sapiens"
/ Ab_xref="taxon:9606"
//Lisue_type="kidney"
// 181
// 182
// Codon_start=1
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Pred. No. 3.3e-216;
0; Mismatches 14;
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1364. .1531
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/product="Epithelin 1 & 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="pot. glycosylation
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1628. .1630
/note="pot. glycosylation
691 c 639 g 428
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/note="cysteine motif 1"
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1595. .1762
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98.5%;
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Plowman, G.D.
Direct Submission
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Best Local Similarity 98.5
Matches 1023; Conservative
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ORIGIN
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AUTHORS
                                                                                                                                                                                                                 TITLE
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                                                             AUTHORS
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FEATURES
                                                                                                 TITLE
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                                                               GAAGTGGTCTCTGCCCCAGCCTGCCACCTTCCTGGCCCGTAGCCCTCACGTGGGTGTGAAG 1582
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       aggtggggcctcaatctaaggcccttccctgtcagaagggggttgaggcaaaagcc-cat
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                                          toggaccaccagcactgctgcccccagcgatacacgtgtgtagctgaggggcagtgtcag
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RESULT AF055008	DEFINITION ACCESSION VERSION KEYWORDS	SOURCE ORGANISM	REFERENCE AUTHORS TITLE JOURNAL	MEDLINE REFERENCE AUTHORS	TITLE JOURNAL MEDLINE REFERENCE	TITLE JOURNAL	SOUL		CDS				BASE COUN	OKIGIN Query M	Matches Qy 1	10	UY 61 Db 1134	
cca 60 	icc 120 	.gc 180 	240 	cc 300 	egc 360 	Jat 420 171	aag 480 AAG 1531	aag 540 AAG 1591	aac 600 AAC 1651	cac 660 	gcc 720 	gta 780 GTA 1831	cct 840 	999 900 	cat 959 Car 2010	101	ATC 20/0	
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Oy 1 Db 1052	Oy 61 Db 1112	Qy 121 Db 1172	Oy 181 Db 1232	Oy 241 Db 1292	Qy 301 Db 1352	Qy 361 Db 1412	Qy 421 Db 1472	Oy 481 Db 1532	Oy 541 Db 1592	Oy 601 Db 1652	Qy 661 Db 1712	Qy 721 Db 1772	Qy 781 Db 1832	Qy 841 Db 1892	Qy 901		Db 2011	Db 2071

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STOCELDESKYGCCPHORATCSDHLHGCPQÖYYCDLIQSKCLSKENATYDLITKLPA
HTVGDVRCDNEWSCPDGTTCCRLQSGAMGCCPPTQAVCCBHIHCCPAGFTCDTQNGT
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                    PRI 02-APR-1998
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Submitted (23-MAR-1998) Molecular and Human Genetics, Baylor
Submitted (23-MAR-1998) Molecular and Human Genetics, Baylor
College of Medicine, One Baylor Plaza S930, Houston, TX 77030, USA
Location/Qualifiers
1. 2178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="similar to Homo sapiens epithelin 1 and 2 encoded by GenBank Accession Number X62320" /codon_start=1
                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalįa; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Yu,W., Andersson,B., Worley,R.C., Muzny,D.M., Ding,Y., Liu,W.,
Ricafrente,J.Y., Wentland,M.A., Lennon,G. and Gibbs,R.A.
Large-scale concatenation cDNA sequencing
Genome Res. 7 (4), 353-358 (1997)

$7264341

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Yu,W. and Gibbs,R.A.
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AF055008 24720 epithelin 1 and 2 mRNA, complete cds.
AF055008
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/clone_lib="lNIB"
/dev_stage="infant"
63. .1844
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Euteleostomi;

Craniata; Vertebrata; I Catarrhini; Hominidae;

Mammalia; Eutheria; Primates;

REFERENCE

Chordata;

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1. 2157
/note="highly similar to AF055008 Homo sapiens clone 24720
epithelin 1 and 2 mRNA"
a 691 c 639 g 428 t
                                                                                                                                             Submitted (15-FEB-2000) to the DDBJ/EMBL/GenBank databases. Sumio Sugano; Institute of Medical Science, University of Tokyo, Deptment of Virology; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
1 (sites)
Matanabe, Kumagal, A., Itakura, S., Yamazaki, M., Tashiro, H.,
Ota, T., Suzuki, Y., Obayashi, M., Nishi, T., Shibahara, T., Tanaka, T.,
Nakamura, Y., Isogai, T. and Sugano, S.
Nakamura, Y., Isogai, T. and Sugano, S.
Unpublished (2000)
2 (bases 1 to 2157)
                                                                                                                                                                                                                        NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5' - & 3'-end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology
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                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
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/cell_line="KATO III"
/cell_type="signet-ring cell carci/clone="KATO")521"
/clone="KATO")521"
/clone="RATO")721"
/clone="cloning vector pMEIBSFL3"
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Pred. No. 7.7e-216;
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98.4%;
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oligo capping; fis (full insert sequence).
Homo sapiens signet-ring cell carcinoma cell_line:KATO mRNA, clone_lib:KAT clone:KAT07521.
Homo sapiens

ORGANISM

AK000607.1 GI:7020815

DEFINITION

LOCUS

RESULT AK000607

ACCESSION VERSION

KEYWORDS SOURCE

AK000607 2157 bp mRNA linear PRI 22-FEB-2000 Homo sapiens cDNA FL/220600 fis, clone KAT07521, highly similar to AF055008 Homo sapiens clone 24720 epithelin l and 2 mRNA.

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85. .1326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRI 31-AUG-2001
highly similar
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I (bases 1 to 1630)
Isogal, T., Ota., T., Hayashi, K., Sugiyama, T., Otsuki, T., Suzuki, Y., Nishikawa T., Nagai, R., Sato, H., Sugano, S., Shiratori, A., Sudo, H., Sugawara, M., Takahashi, M., Chiba, Y., Ishida, S., Murakawa, K., Ono, Y., Takipuchi, S., Watanabe, S., Kimura, K., Murakawa, K., Ishil, S., Rawai, Y., Saito, K., Yamamoto, J., Wakamura, Y., Nagahari, K., Masuho, Y., Ninomiya, K. and Iwayanagi, T., Nabo, human cDNA sequencing project
                                                                                                                                                                                                                                                                                                                                                                                              oligo capping; fis (full insert sequence).
Homo sapiens ovary, tumor tissue cDNA to mRNA, clone_lib:OVARC1
clone:OVARC1001154.
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qai, T. and Otsuki, T.
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/protein_id="BAB14535.1"
/db_xref="G1:10435244"
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/dramslation="MAITAAHGSTAVQTGDPASKDQVTTPWVPSSALIVSSNARTSP
/dramslation="Property of the content of t
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DHQHCCPQGYTCVAEGQCQRGSEIVAGLEKWPARRASLSHPRDIGCDQHTSCPVGQYC
CPSLGGSWARCQLPHAVCCEDRQHCCPAGYTCNVKARSCEKEVVSAQPATFLARSPHY
GVRDVPGGEGHFCHPNQTCCRDNRQGWACCFYRQGVCCADRRHCCPAGFRCAARGTKC
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NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5′- 6 3′-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.
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/organism-"Homo sapiens"
/db.xref="taxon:9606"
/clone="OVARC1001154"
/tissue_type="ovary, tumor tissue"
/clone_lib-"ovary, tumor tissue"
/note="cloning vector: pME185FL3"
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Pred. No. 1.8e-215;
); Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="unnamed protein product"
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TITLE
JOURNAL
FEATURES
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                     AGCACCTCTCCCTAACCAAATTCTCCCTGGACCCCATTCTGAGCTCCCCATCACCATGGG 1455
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               gacgtggagtgtggggaaggacacttctgccatgataaccagacctgctgccgagacaac
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Pred. No. 3.2e-160;
0; Mismatches 13;
                                                                                                                                                                                                                                                                                                     DNA
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Shoyab, M. and Plowman, G.D.
DNA encoding epithelins
Patent: US 5965723-A 3 12-OCT-1999;
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US 5965723.
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578 c 547 g
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Best Local Similarity 98.3%;
Matches 755; Conservative
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AR079655
LOCUS
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Pred. No. 3.2e-160;
0; Mismatches 13;
                                                                                                  DNA
                                                                                                                                                                                               Unclassified.

1 (bases 1 to 1779)
Shoyab, M. and Plowman, G.D.
Epithelins: novel cysteine-rich gro
Patent: US 5416192-A 3 16-MAY-1995;
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US 5416192
                                                                                                                                                                                                                                                                                                /organism="unknown"
578 c 547 g
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II1830
II1830.1 GI:909273
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98.3%;
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Matches 755; Conservative
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Submitted (31-0CT-1997) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 193488)
Birren, B., Fasman, K., McKernan, K., Nusbaum, C., Richardbon, P.,
Lander, E., Allen, N., Baker, J., Baldwin, J., Barna, N., Beckerly, R.,
Boutwell, C., Byrne, S., Cantu, C., Castle, A., Cooke, P., Daly, M.J.,
Depayre, E., Devon, K., Dewar, K., Dukette, B., Etemadi, S.,
Ferreira, P., Forrest, C., Gage, D., Gardyna, S., Gensheimer, S.,
Geraigery, K., Gilmartin, T., Gray, D., Hagos, B., Harris, K.,
Horton, L., Howland, J.C., Hui, L., Jacotot, L., Linton, L.,
Mackenzie, J., Marquis, M., McEwan, P., McGurk, A., Maldrim, J.,
Molla, M., Morris, M., Morrow, J., Nachman, A., Naylor, J., O'Connor, T.,
Pavlin, B., Peterson, R., Ranganath, S., Riley, R., Roberts, D.,
Stone, C., Strickland, C., Sydney, K., Shyam, R., Sochoo, S., Stilwell, J.,
Stone, C., Strickland, C., Sydney, K., Tang, L., Vassiliev, H., Vo, A.,
Magner, A., Wheeler, J., Wu, Y., Ye, W. J., Zemtseva, I., Zhao, J. and
Peterson, K., Roberts, D., Rollins, G., Sarnaik, A., Shiu, P., Shyam, R., Stliwell, J., Stone, C., Strickland, C., Sydney, K., Tang, L., Zemtseva, I. and Zody, M.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (03-FEB-1998) Whitehead Institute/MIT Center for Ge
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Feb 3, 1998 this sequence version replaced gi:2673895.
The Staden databases, finishing information, and all
chromatographic files used in the assembly of this clone are
available from our anonymous ftp site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               All repeats were identified using RepeatMasker: Smit, A.F.A. Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html.
LocatLon/Wallifiers
1. .139488
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="17"
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//clone_lib="Peter de Jong/ human PAC library"
19. .233
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/rpt_famlly="AluSp"
complement (1044. .1346)
/rpt_famlly="AluSq"
1627. .1788
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5911. 6078
/rpt_family="AluSg/x"
6080. 6110
/rpt_family="(GAAA)n"
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/rpt_family "AT_rich"
10525. .10566
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10958. .11093
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/rpt_family="LTR16A"
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6660. .6946
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035, .9334
rpt_family="AluSx"
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rpt_family="AluJo"
962. .7252
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'Tpt_family="MIR"
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2 (bases 1 to 139488)

Birren, B., Fasman, K., McKernan, K., Munro, C., Nusbaum, C., Chang, A., Richardson, P., Lander, E., Baldwin, J., Barna, N., Cantu, C., Chang, A., Cooke, P., Daly, M., Davon, K., Dewar, K., DuRette, B., Forrest, C., Gage, D., Gensheimer, S., Geraigery, K., Gilmartin, T., Hagos, B., Halphen, I., Harris, K., Howland, J.C., Huang, J., Hui, L., Jacotot, L., Kirby, A., Lane, M., MacKenzie, J., Marquis, N., McDermott, J., Molla, M., Morrow, J., Nachman, A., Naylor, J., O'Connor, T., Olotu, A.,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Birren,B., Fasman,K., McKernan,K., Nusbaum,C., Richardson,P. and
Lander,E.
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Homo saplens chromosome 17, clone HRPC1067M6, complete sequence.
AC003043
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           caagcettgaagagatgteceetgtgataatgteageagetgteceteeteegatace
                                 1072 CAAGCCTTGAAGAGAGAGATGTCCCCTGTGATAATGTCAGCAGCTGTCCCTCCTCCGGTACC
                                                                                                 tgctgccaactcacgtctggggagtggggtgctgctgtccaatcccagaggctgtctgctgctgc
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	ps 216	36525 276 36465	336 36405 396 36345	402 36285 424 36225	484 36165 544 36105 604 36045
塔	19th 139488; Jels 183; Ga	GCTACACG agaagatg 	acaccagc ACACCAGC gccagttg 	GAGGGGAC ggatcgcc 	gaaggaag
	Length Indels	cccccagg tggactgg 	ccttatcccacccagagacatcggctgtgaccagcaccagc 	AGGGAGCTAAGCCCAGTGAGGGACACgctgtgtgctgcgagagatcgcc	atcctgcga ArcreceGA ArcreceGA 39tgggtgt
9) 0) 7) 7) 4) ~\{ 5) coverage." 3) 3)	; DB 9; .5e-133; es 18; gcactgctg	gategtgge 	categgete 	GGGGAGCTI	aaggetegi
54 69 69 191 191 191 191 191	re 629.2; d. No. 1. Mismatche gaccaccag	igaccacca iggaagcga 	cccagaga 	CCCCTGGATA	gcaacgtg
0. 0004030014412H 13883H3112H H71	.1%; Score .1%; Pred. e 0; Mis tgctgctcggac	rGCTGCTCG Egtcagcga 	ttatcccac 	CTGCCTGCC	gctacacct
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Qy 605 agggctgggcctgctgccta	756 gagacagctgctgtgaggacagtactgaagactctgcagccctcgggacccactcggacccactcggacccactcggacccactcggacccactcggacccactcggacccactcggacccactcggacccactcggacccactcgacactcgacactcacacactcgacactcacacactcgacacccactcgacacactcaccacactcacacactcacacactcacacactcacacactcacacactcacacactcacacactcacacactcacacactcacacactcacacactcacacactcacacacacacacacacacacacacacacacacacacaca	ે. જે દેશ નેન	a a a

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NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                    Quality coverage: 7.04 in Q20 bases; agarose-fp
Quality coverage: 7.13 in Q20 bases; sum-of-contigs
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of 10095 bp in length
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of 1092 bp in length
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                                                               Assembly program: Phrap; version 0.990319
Consensus quality: 174306 bases at least Q40
Consensus quality: 176607 bases at least Q30
Consensus quality: 177668 bases at least Q20
Insert size: 181000; agarose-fp
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/note="assembly_name:Contig33"
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/note="assembly_name:Cont1g34"
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'note="assembly_name:Contig32
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 180520)
Waterston,R.H.
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Submitted (30-DEC-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
MO 63108, USA
On Jun 17, 2000 this sequence version replaced gi:7524009.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          529 gtgggtgtgaaggacgtggagtgtggggaaggacacttctgccatgataaccagacctgc
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Web site:http://genome.wustl.edu/gsc/index.shtml
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Mammalia, Eutheria, Primates,
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Waterston, R.H.
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Waterston, R.H.
Direct Submission
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Pred. No. 4.5e-126;
0; Mismatches 16;
               vector_side:right"
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70te="assembly_name:Contig40"
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         clone_end:T7
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DNA linear HTG 23-FEB-2000
*** SEQUENCING IN PROGRESS ***, 46
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Catarrhini; Hominidae; Homo.
           13764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (30-DEC-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
On Feb 23, 2000 this sequence version replaced gi:6648373.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
* NOTE: This is a 'working draft' sequence. It currently a consists of 46 contigs. The true order of the pleces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center: Washington University Genome Sequencing Center Center code: WUGSC
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                                              Indels 185
                                    Length 189391;
             5392 others
                                    Score 565; DB 2; I
Pred. No. 6.5e-119;
0; Mismatches 35;
/db_xref="taxon:9606"
/clone="RP11-811N11"
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Conservative
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/note="cysteine motif 5"

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VNEWKCDLEVSCPGSTTCCRLNTGAMGCCPFTKAVCCEDH HCCPAGFQCHTETGTCE
LGVLQVPMMCKTASLSLPDPQILKNDVPCDDFSSCPSNNTCCRLSSGDMGCCPIPEA
VCCLDHQHCCPQGFKCMDESYCQKGDRWVAGLEKMPVRQTTLLAGHGDIGCDQHTSCPV
GQTCCPSLKGSWACCQLPHAYCCEDRQHCCPRATTCNYKARTCEKDAGSYQPSMDLF
GSKVGNVECGAGHFCHDNQSCCKDSQGGWACCPYVKGVCCRDGRHCCPIGFHCSAKGT
                                                                                                                                                                                   X62322.1 GI:56108
epithelial cell growth regulator; Epithelin 1; Epithelin 2; soluble
                                                                                                                                              ROD 26-AUG-1992
                                                                                                                                                                                                                                                    Chordata; Craniata; Vertebrata; Euteleostomi;
Rodentia; Sciurognathi; Muridae; Murinae;
 Direct Submission
Submitted (15-7AN-1991) G.D. Plowman, Oncogen, 3005 1st Avenue,
Seattle, WA 98121, U S A
See also X62320-2.
                                                                                                                                                                                                                                                                                           1 (bases 1 to 2153)
Plowman,G.D., Green,J.M., Neubauer,M.G., Buckley,S.D.,
McDonald,V.L., Todaro,G.J. and Shoyab,M.
The epithelin precursor encodes two proteins with opposing activities on epithelial cell growth
J. Biol. Chem. 267 (18), 13073-13078 (1992)
                                                                                                                                               linear
                                                    .42. .144
/note="pot. glycosylation site"
                                                                                                                                        2153 bp mRNA R.norvegicus mRNA for epithelin 1 and 2. X62322
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/organism="Rattus norvegicus"
/db_xref="taxon:10116"
/tissue_type="Kidney"
/clone_lib="lambda gt10"
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/product="Epithelin 1 & 2"
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/note="cysteine motif 1
397. .567
/note="cysteine motif 2
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368. .1035
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Rattus norvegicus
Eukaryota; Metazoa; C
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Plowman, G.D.
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                                                                                                                                          Length 2153;
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                                                                                                                                                                    264; Indels
                                                                                                                                          Score 560.6; DB 10;
Pred. No. 1.1e-117;
              site"
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/// ... 1/49
// note="pot. glycosylation si
// note="cysteine motif 6"
// note="cysteine motif 6"
// note="cysteine motif 7"
// note="cysteine motif 7"
// note="pot. glycosylation si
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73.5%;
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/function="putative growth factor precursor"
/function="putative growth factor precursor"
/note="The precursor contains the sequence of rat granulin
/Rateman,A.et al. BBRC (1990),173,1161-1168) / epithelin
land epithelin 2 (Shoyab,M.et al.(1990) PNAS 87,
7912-7916)
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LLDTWPITTSRRLDGSCQIRDHCPDGTSCLLTVSGTSSCCPPSEGVSCDGGGGCPRG
FRCSADGRSCSQISDSLLGAVQCPGSQFECPDSATCIMIDGSWGCCPMPQASCCEDR
VHCCPHGASCDLVHFRCISFTGTHFLIKKFPAQRTNRAVASFSVVCPDAKTQCPDDST
CCELPTGKTGCCPMPNAICCSDHLHCCPQDTVCDLIQSKCISKDYTTDLATKLPGTPV
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SKVGNVECGAGHFCHDNQSCCKDSQGGWACCPYVKGVCCRDGRHCCPIGFHCSAKGTK
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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epithelin; granulin.
Rattus norvegicus (strain Sprague-Dawley) (library: lambda-gtll)
adult kidney cDNA to mRNA.
Rattus norvegicus
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ctccctagcacctcccctaaccaaattctcctggaccccattctgag-ctcccatca
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Bhandari,Y., Glaid,A. and Bateman,A.
The complementary decoyribonucleic acid sequence, tissue distribution, and cellular localization of the rat granul
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/organism="Rattus norvegicus"
/db_xref="taxon:10116"
1. 2113
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/db_xref="GI:204224"
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/note="putative"
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Pred. No. 6.16\117;
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/function-"growth factor"
/product-"granulin B/epithelin
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/gene-"granulin"
/note-"putative"
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GP88; granulin; epithilin; human; growth factor; autocrine; tumour; cancer; viral infection; antagonist; therapy; diagnosis; ss.
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Mouse GP88 autocri
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                             GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                              Composition containing antagonist of growth factor GPB8 - useful for treating cancer and viral diseases and also for diagnosing disease from altered GPB8 expression
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Pred. No. 4.9e-270;
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Best Local Similarity 99.9%;
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healing; inhibition; peptide;
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/transl_except= ATG encodes Valine.
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topically
                            The granulin inhibits keratinocytes and for promoting the healing of wounds.
              English
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                                                                                                                                                                                                                                                                                                                                        Granulin; keratinocytes; wound healing; inhibition; peptide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         granulin inhibits keratinocytes and is useful in promoting the healing of wounds.
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Pred. No. 5e-270;
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A*tag a /*taga a //transl_except ATG misc_difference 1714..1716
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0;

cancer associated gene sequence SEQ ID NO:574

08-FEB-2001

Human

cancer associated gene; cancer

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in AAB4339 to AAB44239. The proteins can have activities based on the tissues and cells the genes are expressed in. Example of activities include: cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antiallergic; antiarthritic; antidiabetic; antiasthmatic; antiallergic; antiarthritic; antidiabetic; antiasthmatic; antiallergic; antibacterial; antiviral; dermatological; neuroprotective; cardiant; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic and antianglogenic. The polynucleotides and polypeptides can be used for preventing, treating or meliorating medical conditions and diagnosing pathological conditions. Polynucleotides, polypeptides, antibodies, agonists and antagonists from the present invention may be used to treat immune disorders by activating or inhibiting the proliferation, differentiation or mobilisation of immune cells, to treat disorders of haematopoletic cells, autoimmune disorders, allergic reactions, graft versus host disease and organ rejection, modulate haemostatic or thrombolytic activity, modulate infeations. The peptides, nucleotides, antibodies, agonists and antagonists may be also be used in drug screens. AAC78449 to the control of the
                                                                                                                diagnosis; cytostatic; proliferative; vulnerary; immunomodilator; antidabetic; antiasthmatic; antirheumatic; antidarthritic; antiditamatic; antidarthritic; antidathritic; antidathritic; antidathritic; dermatological; neuroprotective; thrombolytic; coaqulant; noctropic; vasotropic; antipsorlatic; antidangiogenic; gene therapy; inflammation; immune disorder; haematopoletic cell disorder; autoimmune disorder; antidatic; antidatic cell disorder; autoimmune disorder; haematopoletic call disorder; autoimmune disorder; haemostatic; cardiovascular disorder; infection; neurological disease; drug screening; ås.
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                                                                                   antigen; detection; cancer;
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Pred. No. 1.1e-249;
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standard; cDNA; 2432

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AAC78180

CDNA sequence SEQ ID NO:15309

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The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of oligonucleotide comprises at least 15 nucleotides and the combination of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length and AAH13633 to AAH13633 to AAH13633 to AAH13633 to AAH13633 to AAH13633 to AAH13633 and AAH13633 to AAH13632 to AAH13632
                                               SS.
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                                           Human; primer; detection; diagnosis; antisense therapy; gene therapy;
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Otsuki
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Pred. No. 6.9e-249;
0; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 8; SEQ ID 15309; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                    Nagai K,
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A, Naga
                                                                                                                                                                                                                                                                                                                                                    Nishikawa T,
Y, Wakamatsu
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99JP-0300253.
2000JP-0118776.
2000JP-0183767.
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Best Local Similarity 98.3
Matches 1021; Conservative
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                                                                                                                                                                                                                                                                                                                                                                    Sugiyama
                                                                                                                                                                                                                                                                                                                                                    Isogai Tr.
                                                                                                                                                                                                               29-JUL-1999;
27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
                                                                                Homo sapiens
                                                                                                                EP1074617-A2
                                                                                                                                                                                 28-JUL-2000;
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AAH16370 RESULT

26-JUN-2001 AAH16370; AAH16370

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ET-1 and ET-2 were isolated from rat kidneys and their amino acid sequences determined. A full length rat ET cDNA (AAQ14338) was obtd. by screening a rat kidney cDNA library in lambda gill0 with PCR generated ET probes. These probes were also used to obtain the mouse ET gene (AAQ14340) from a mouse T-cell genomic library.

ET DNA was also obtained from human sources (AAQ14339).

An anti-sense ribonucleic amine sources (AAQ14339).

An anti-sense ribonucleic arid molecule complementary to the indicated fragment in the features is also claimed.

ET-1 is a bifunctional growth regulator, capable of stimulating the growth of some cell types while inhibiting the growth of some cell types while inhibiting the growth of some cell types will a further in the decivity. In contrast, however, ET-2 is apparently not capable of eliciting the growth stimulatory activity characteristic of ET-1 and, in fact, antagonises this ET-1 activity.

See also AAQ14338-40, AAQ14952-53, AAR14328-9 and AAR15315-20.
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                                                                                         Mi.
                                                                                                                                                                                                                                                                                                                                         New cysteine-rich growth modulating proteins, epithelins - us as inhibitors of neoplastic cell growth and to promote wound healing and treat psoriasis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 12;
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Pred. No. 1.5e-185;
0; Mismatches 13;
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"claim 9, page
                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 22; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cch 69.7%;
il Similarity 98.3%;
755; Conservative
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                                                                                                                                                                          03-APR-1991;
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                          Homo sapiens
                                                                                                                                               17-0CT-1991.
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Human epithelin precursor.

17-JAN-1992

AAQ14339

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                                                                                                                                                                                                                                                                                                                                                                                                          GP88; granulin; epithilin; mouse; growth factor; autocrine; tumour; cancer; viral infection; antagonist; therapy; diagnosis; ss.
                                             cgacagggctgggcctgctgtccctaccgccagggcgtctgttgtgctgatcggcgccac
                                                                                                            gaagtggtctctgcccagcctgccaccttcctggcccgtagccctcacgtgggtgtgaag
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Caccccagagacatcggctgtgaccagcaccagctgccggtgggcggaacctgctgc
                                   ccgagccagggtgggagctgggcctgctgccagttgccccatgctgtgtgctgcgaggat
                                                                                                                       /*tag= a
/transl_except= (pos:44..45, aa:11e)
/transl_except= (pos:182..184, aa:Asp)
/transl_except= (pos:1151..1153, aa:Cys)
/transl_except= (pos:1340..1342, aa:Leu)
                                                                                                                                                                                                                                                                                                                                                                                         Mouse GP88 autocrine growth factor cDNA
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23..1792
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97US-0863079.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAW85474.
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23-MAY-1997;
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This murine cDNA sequence includes a coding region for GPB8 (see AAW85474), an 88 kDa glycoprotein autocrine growth factor and epithilin/granulin precursor that is expressed in a tightly epithilin/granulin precursor that is expressed and unregulated in highly tumprigenic cells derived from normal cells, and which acts as a stringentic cells derived from normal cells, and which tumorigenic cells. Inhibition of GPB8 expression or action in the tumorigenic cells results in an inhibition of the tumorigenic cells results to an inhibition of the tumorigenic cells results to an inhibition of the tumorigenic cells as probe obtained by PCR using primers, based on isolated GPB8 ceptides. Antagonists to GPB8 are used to treat diseases associated with increased expression of GPB8, particularly cancer but also viral infections. Fragments of GPB8, particularly cancer but also viral infections. Fragments of GPB8, particularly cancer cells) and to screen for antibodies. Antiseases antagonists, as diagnostic reagents cells) and to screen for antibodies. Antisease oligonucleotides can also be used as antagonists. Methods are provided for resulting from altered GPB8 activity.
factor GP88 - useful for for diagnosing disease
Composition containing antagonist of growth treating cancer and viral diseases and also
                                                                                                               Example 5; Fig 8A-D; 86pp; English.
                                                             from altered GP88 expression
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Sequence 2137 BP; 443 A; 608 C; 583 G; 503 T; 0 other;

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                                  gggcccaccaggtgcctggatggagaaggccccagctcacctcagcctgccagaccca
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Length 2137;
                 15;
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Score 535.4; DB 20;
Pred. No. 3.8e-130;
0; Mismatches 281;
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Best Local Similarity 71.9%;
Matches 759; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunogenic portion of an ovarian carcinoma protein and the nucleic acid encoding it, useful for the diagnosis, prevention and treatment cancer, preferably ovarian cancer.
                                                                                                                                                                                                                                                                                                                                                               carcinoma; ovarian cancer; therapy; diagnosis;
identification; cytostatic; gene therapy; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes an isolated polypeptide comprising
                                      tgetgteetgetggetteegetgegeaegeaggggtaeeaagtgtttgegeagggagee
      ogacagggctggtctgtcctacgcccagggcgtctgttgtgctgatcggcgccac
                                                                                                                                       cctccctagcacctccccctaaccaaattctccctggaccccattctgag-ctccccatc
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                                                                                                     781 ctgaa----gactctgcagccctcgggaccccactcggagggtgccctctgctcagg
                                                                       ccgcgctgggacgccctttgagggacccagccttgagacagctgctgtgagggacagta
                                                                                                                                                                                                                                                                                                                                               Human ovarian carcinoma antigen polynucleotide SEQ ID NO:89.
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98US-0216003.
99US-0338933.
99US-0404879.
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                                                                                                                                                                                                                                                                                      AAA69779/c
ID AAA69779 standard; cDNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORP.
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                                                                                                                                                                                                                                                                                                                                                                       tumour antigen;
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                                                                                                                                                                                                                                                                                                                                                                Human; ovarian
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24-SEP-1999;
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immunogenic portion of an ovarian carcinoma protein (or its variants). Ovarian carcinoma proteins, and polynucleotides encoding them, have cytostatic activity and can be used in gene therapy and vaccines. Ovarian carcinoma polypeptides, nucleic acids, antibodies and vaccines are useful for the prevention, diagnosis and treatment of cancer, preferably ovarian cancer. ANA69691 to ANA70177 and AAB12552 to AAB12557 represent human ovarian carcinoma polynucleotides and proteins used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                              626
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                                                                                                                                                                                                                                                    3;
                                                                                                                                                                                                                 Length 561;
                                                                                                                                                                                                                                                    Indels
                                                                                                                                                             Sequence 561 BP; 124 A; 163 C; 176 G; 96 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RNA; growth regulation; inhibition;
                                                                                                                                                                                                             Score 483.8; DB 21;
Pred. No. 7.8e-117;
0; Mismatches 9; 1
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/note= "claim 19, page
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31..1797
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                                                                                                                                                                                                                 45.1%;
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                                                                                                                                                                                                               Query Match
Best Local Similarity 97.7
Matches 521; Conservative
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ET; anti-sense
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misc_RNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ttagaccaccagcattgctgccctcagggtttcaaatgtatggatgaggggtactgtcag 1245
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                                                                                                                                                                                                                                                                                                                                                               of
                                                                                                                                                                                                                                                                                                      An anti-sense ribonucleic acid molecule complementary to the indicated fragment in the features is also claimed.

Err-1 is a bifunctional growth regulator, capable of stimulating the growth of some cell types while inhibiting the growth of others.

Err-2 is functionally similar to Er-1 w.r.t. growth inhibitory bloactivity. In contrast, however, Er-2 is apparently not capable of eliciting the growth stimulatory activity characteristic of Er-1 and,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 gggccccaccaggtgccctggatggagaaggccccagctcacctcagcctgccagaccca 60
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                                                                                                                                                                                                                                     ET-2 were isolated from rat kidneys and their amino acid
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                                                                                                                                                                                                                                                                                                                                                                                      in fact, antagonises this ET-1 activity.
See also AAQ14338-40, AAQ14952-53, AAR14328-9 and AAR15315-20.
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1767 BP; 359 A; 499 C; 491 G; 418 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      43.8%; Score 469.2; DB 12; 76.7%; Pred. No. 7.3e-113; Live 0; Mismatches 173;
                                                                                                                                                                                                              Disclosure; Fig 18; 97pp; English.
                                                                                      (BRIM.) BRISTOL-MYERS SQUIB.
                               91WO-US02321
                                                    91US-0083796
90US-0504508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity (0., Matches 589; Conservative
                                                                                                             Shoyab M, Plowman GD;
                                                                                                                                 1991-325168/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                           P-PSDB; AAR14325.
                               03-APR-1991;
                                                    13-MAR-1991;
03-APR-1990;
          17-0CT-1991
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1486 gatgcaggctctgtccagccttccatggacctgacctttggctctaaggttgg----g
                                                                                                                                                                                                           541 gacgtggagtgtggggaaggacacttctgccatgataaccagacctgctgccgagacaac
                                                                                                                                                                                                                                                                                                                           601 cgacagggctgggcctgctgtcctacgcccagggcgtctgttgtgctgatcggcgcac
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/note= "claim 29, page
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8..1774
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P-PSDB; AAR14327.
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Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.

sapiens.

Ношо

WO9514772-A1 01-JUN-1995.

gene signature HUMGS03681

Human

(first entry)

02-AUG-1996

7.

94WO-JP01916 93JP-0355504

11-NOV-1994; 12-NOV-1993; Okubo\K;

Matsubara K,

MATS/) MATSUBARA K. (OKUB/) OKUBO K WPI; 1995-206931/27.

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ET-1 is a bifunctional growth regulator, capable of stimulating the growth of some cell types while inhibiting the growth of others. ET-2 is functionally similar to ET-1 w.r.t. growth inhibitiory bloactivity. In contrast, however, ET-2 is apparently not capable of eliciting the growth stimulatory activity characteristic of ET-1 and, in fact, antegonises this ET-1 activity.

See also AAQ14338-40, AAQ14952-53, AAR14328-9 and AAR15315-20.
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                                                                                                                                                   Score 448.4; DB 12; Length
Pred. No. 2e-107;
0; Mismatches 186; Indels
                                                                                                            Sequence 1767 BP; 360 A; 503 C; 492 G; 412 T; 0 other;
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                                                                                                                                                    41.8%;
75.0%;
                                                                                                                                                                              576; Conservative
                                                                                                                                                                   Similarity
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A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 '6S" sequences given in AAT19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA libraries prepared of mRNA by using poly(T) as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gatoggogceactgctgtcctgctgctgctccgctgcgcacgcagggtaccaagtgttg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        taagggacagtactgaagactctgcagcctcggnaccccactcggagggtgccctctgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 catcaccatgggaggtggggcctcaatctaaggcccttccctgtcagaagggggttgagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tcaggcctccctagcacctcccctaaccaaattctccctggaccccattctgagctccc
                                                                                                                                                                                                                                                                                                                                                                             Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 339.2; DB 16; Length
Pred. No. 4.7e-79;
0; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G; 101 T; 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 1045; 2245pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 439 BP; 79 A; 133 C; 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 31.6%;
Best Local Similarity 95.1%;
Matches 366; Conservative
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AAT22115 standard; cDNA to mRNA; 439

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RESULT

AAT22115

AAT22115;

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AAK18681;

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RESULT 12 AAK18681/c

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This invention describes a novel gene library (A) comprises a gene sequence (or its part) encoding a protein involved in amino acid synthesis, cellular/energy metabolism, metabolism of fatty acids/phospholipids, synthesis or breakdown of purines/pyrimidines/nucleosides/nucleotides, DNA replication/transcription/translation, or is a transport/binding protein. (A) are produced that correspond to the 3'-end of mRNA but without the polyA tail. They can be prepared more efficiently and with less effort than conventional libraries. AAK53436-AAK54275 represent fragments of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene library containing sequences with specific 3'-ends and no polyA tail, encoding proteins involved in a wide range of cellular processes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Murine; liver; gene/library; amino acid synthesis; binding protein; cell metabolism; energy metabolism; fatty acid metabolism; synthesis; phospholipid metabolism; purine; pyrimidine; nucleoside; nucleotide; replication; transcription; translation; transport protein; ss.
113 GCTCGATCCTGCGAGAAGGAAGTGGTCTCTGCCCAGCCTGCCACCTTCCTGGCCGTAGC 114
                                                                                                                                                                                                                                                                                                                                                                                                       Murine transport and binding associated protein encoding cDNA SEQ ID
                                                              523 cctcacgtgggtgtgaaggacgtggagtgtggggaaggacacttctgccatgataaccag
                                                                                 113 CCTCACGTGGGTGTGAAGGACGTGGACGTGTGGGGAAGGACGACACTTCTGCCATGATAACCAG
                                                                                                                                      583 acctgctgccgagacaaccgacagggctgggcctgctgtccctacgcccagg 634
                                                                                                                                                           19.3%; Score 206.6; DB 22; Length 68.0%; Pred. No. 2.4e-44; 1.1ve 0; Mismatches 154; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene library described in the method of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 15; Page 42; 251pp; German.
                                                                                                                                                                                                                                                                                    BP.
                                                                                                                                                                                                                                                                                    AAK53492 standard; cDNA; 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2001; 2001DE-2003510.
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                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 349; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DE20103510-U1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-JUN-2001.
                                                                                                                                                                                                                                                                                                                          AAK53492;
                                                                                                                                                                                                                                            RESULT 13
AAK53492/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Single exon nucleic acid probes for analyzing gene expression in human brains.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 present invention provides a number of single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; brain expressed exon; gene expression analysis; probe; microarray; Alzhelmer's disease; multiple sclerosis; schizophrenia;
                         catcaccatgggaggtggggcctcaatctaaggc-cttccctgtaagaagggggttgtgg
    Example 4; SEQ ID NO: 18672; 650pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                              expressed single exon probe SEQ ID NO: 18672.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 233 BP; 43 A; 75 C; 73 G; 42 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chen W, Rank DR;
                                                                                                                                            1008 ctttccctatccacaggggtgtt 1032
                                                                                                                                                                 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-FEB-2000; 2000US-0180312.
26-MAY-2000; 2000US-0207456.
30-UNA-2000; 2000US-068408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234687.
04-OCT-2000; 2000GS-0024263.
                                                                                                                                                                                                                                                                                  AAK18681 standard; DNA; 233
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                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             epilepsy; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-483446/52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200157275-A2.
                                                                                                                                                                                                                                                                                                                                                                    05-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                              Human brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Simi
Matches 230;
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Length 565;

acagggctgggcctgctgtccctacgcccaggcgtctgttgtgtgctgatcggcgccactg 662

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463 getegatectgegagaaggaagtggtetetgeceageetgeeacetteetggeeegtage 522

Query Match

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The invention comprises compositions used for the therapy and diagnosis of ovarian cancer. The compositions comprise one or more ovarian tumour proteins, their associated polynuclectides, or immunogenic portions of the proteins. The ovarian tumour polynucleotides and polypeptides are useful for stimulating and/or expanding T cells specific for a tumour protein. They are also useful for inhibiting the development of cancer in a patient with an ovarian tumour DNA or protein by incubating isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nmunogenic protein; cancer; ovarian tumour; T-cell stimulation; ss;
gene therapy; cytostatic; T-cell expansion; nucleic acid hybridisation;
primer; probe.
                                                                                                                                                                                                                                                                                                            goccattacaagctgccatcccctcccgtttcagtggaccctgtggccaggtgctttc 1013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancer
                                                                                                                         835
                                                                                                                                                                                                                                                953
                                                                                                                                                                                                                                                                205 CATGGGAGGTGGAGCCTCAAAACCTTCTTTATGGAAAGAGGCTGTGGCCAAAA 146
                723 gcgctgggacgccctttgagggacccagccttgagacagctgctgtgagggacagtact 782
                                                                                     266
                                                                                                                                                                                   894
                                                                                                                                                                                                                  265 TCCCTAGCGCCTCCTCCCCTAACGTCTCCCCGGCCTACTCATCCTGAGTCACCCTATCAC 206
                                                                                                                                                                                                                                                                                                                                           86
                                                                                                                                                                                   tecetageacetececetaaceaaattetecetggaceceattetgag-etececateae
                                                                                                                                                                                                                                                  catgggaggtggggcctcaatctaaggcccttccctgtcagaagggggttgagg-caaaa
                                                                                                                                                                                                                                                                                                                                           145 GCCCCGTATCAAACTGCCAFTTCTTCCGGTTTCTGTGGACCTTGTGGCCCAGGTGCTCTTC
                                                                                                                         783 gaa-----gactctgcagccctcgggaccccactcggagggtgccctctgctcaggcc
                                                                                                                                         663 ctgtcctgctggcttccgctgcgcacgcaggggtaccaagtgtttgcgcagggaggcccc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polynucleotides encoding ovarian tumour proteins, useful for treating ovarian cancer, and as probes, primers, and markers of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human ovarian PCR-subtracted cDNA library clone #783.
                                                                                                                                                                                                                                                                                                                                                                         1014 cctatccacaggggtgttgtgtgtgtgggtgg 1046
                                                                                                                                                                                                                                                                                                                                                                                                          23
                                                                                                                                                                                                                                                                                                                                                                                                      85 ccgAccacAcGGTGTTCTGTGAGCTTGCTTGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAS24602 standard; cDNA; 336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-FEB-2001; 2001WO-US03733
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-488879/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mannion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200157207-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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T-cells allowing them to proliferate, and administering to the patient. The sequences can be used as markers for cancer, for example, to monitor ovarian cancer progression. Probes and primers are useful in nucleic acid hybridisation, in detecting the presence of complementary sequences in a given sample, for preparing mutant species and for preparing quber genetic constructions. Sequences AAS23820-AAS25231 and AAS25328-AAS25549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ovarian tumor proteins, and nucleic acids encoding them, used to
                                                                                                                                                                                                                                                                                                                                                                                      943 ttgaggcaaaagcc--cattacaagctgccatccctcccgtttcagtggaccctgtgg 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO:848.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAH82377 to AAH83878 represent human ovarian tumour-associated polynucleotide sequences which encode ovarian tumour proteins. The ovarian tumour protein and polynucleotide sequences have cytostatic activity, and can be used in gene therapy and vaccine production. The ovarian tumour proteins and polynucleotides can be used to inhibit the development of cancer, particularly ovarian cancer. They can also be used to diagnose the onset and progression of cancer.
                                                                                                                                                                                                                                                                        882
                                                                                                                                                                                                                                                                                                                                942
                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                           61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ovarian tumour; ovarian cancer; diagnosis; gene therapy;
                                                                                                                                                    Score 197.8; DB 22; Length 336;
Pred. No. 4e-42;
0; Mismatches 3; Indels 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human ovarian tumour associated polynucleotide sequence
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                                                                                    represent human ovarian tumour protein cDNA clones.
                                                                                                               Sequence 336, BP; 70 A; 87 C; 106 G; 62 T; 11 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 5; Page 219; 338pp; English.
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